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NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	JAN 27	Source of Registration (SR) information in REGISTRY updated and searchable
NEWS	4	JAN 27	A new search aid, the Company Name Thesaurus, available in CA/CAPLUS
NEWS	5	FEB 05	German (DE) application and patent publication number format changes
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NEWS	15	APR 27	NLDB: New search and display fields available
NEWS	16	May 10	PROUSDDR now available on STN
NEWS	17	May 19	PROUSDDR: One FREE connect hour, per account, in both May and June 2004
NEWS	18	May 12	EXTEND option available in structure searching
NEWS	19	May 12	Polymer links for the POLYLINK command completed in REGISTRY
NEWS	20	May 17	FRFULL now available on STN
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=> s heirarchical and non-hierarchical

L1 0 HEIRARCHICAL AND NON-HIERARCHICAL

=> s hierarchical and non-hierarchical

L2 150 HIERARCHICAL AND NON-HIERARCHICAL

=> s l2 and clustering

L3 39 L2 AND CLUSTERING

=> duplicate remove l3

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L4 35 DUPLICATE REMOVE L3 (4 DUPLICATES REMOVED)

=> d 1-35 bib ab

L4 ANSWER 1 OF 35 MEDLINE on STN
AN 2004165716 IN-PROCESS
DN PubMed ID: 15059657
TI Towards realistic description of collective motions in the lattice protein folding models.
AU Yesylevskyy S O; Demchenko A P
CS A.V. Palladin Institute of Biochemistry, Leontovicha Street 9, Kiev 01030, Ukraine.
SO Biophysical chemistry, (2004 Apr 1) 109 (1) 17-40.
Journal code: 0403171. ISSN: 0301-4622.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20040403
Last Updated on STN: 20040430
AB Collective motions and the formation of clusters of residues play an important role in the folding of real proteins. However, existing Monte Carlo (MC) techniques of the protein folding simulations based on highly popular lattice models provide only a schematic representation of collective motions, which is rather far from physical reality. The

Clustering Monte Carlo (CMC) algorithm was developed with particular aim to provide a realistic description of collective motions on the lattice. CMC allows modeling the cluster dynamics and the effects of the solvent viscosity, which is impossible in conventional algorithms. In this study two 2D lattice peptides, with the ground states of **hierarchical** and **non-hierarchical** design, were investigated comparatively using three methods: Metropolis MC with the local move set, Metropolis MC with unspecific rigid rotations and the CMC algorithm. We present evidence that the folding pathways and kinetics of hierarchically folding clustered sequence are not adequately described in conventional MC simulations, and the account for cluster dynamics provided by CMC allows to capture essential features of the folding process. Our data suggest that the methods, which enable specific cluster motions, such as CMC, should be used for a more realistic description of protein folding.

L4 ANSWER 2 OF 35 MEDLINE on STN DUPLICATE 1
 AN 2003173350 MEDLINE
 DN PubMed ID: 12691990
 TI Client-server environment for high-performance gene expression data analysis.
 AU Sturn Alexander; Mlecnik Bernhard; Pieler Roland; Rainer Johannes; Truskaller Thomas; Trajanoski Zlatko
 CS Institute of Biomedical Engineering, Graz University of Technology, Christian Doppler Laboratory for Genomics and Bioinformatics, Krenngasse 37, 8010 Graz, Austria.
 SO Bioinformatics (Oxford, England), (2003 Apr 12) 19 (6) 772-3.
 Journal code: 9808944. ISSN: 1367-4803.
 CY England: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 200312
 ED Entered STN: 20030416
 Last Updated on STN: 20031217
 Entered Medline: 20031216
 AB SUMMARY: We have developed a platform independent, flexible and scalable Java environment for high-performance large-scale gene expression data analysis, which integrates various computational intensive **hierarchical** and **non-hierarchical clustering** algorithms. The environment includes a powerful client for data preparation and results visualization, an application server for computation and an additional administration tool. The package is available free of charge for academic and non-profit institutions.

L4 ANSWER 3 OF 35 MEDLINE on STN DUPLICATE 2
 AN 2003519799 MEDLINE
 DN PubMed ID: 14596807
 TI Parameterization and classification of the protein universe via geometric techniques.
 AU Tendulkar Ashish V; Wangikar Pramod P; Sohoni Milind A; Samant Vivekanand V; Mone Chetan Y
 CS Kanwal Rekhi School of Information Technology, Indian Institute of Technology, Bombay, Powai, Mumbai 400 076, India.
 SO Journal of molecular biology, (2003 Nov 14) 334 (1) 157-72.
 Journal code: 2985088R. ISSN: 0022-2836.

CY England: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 200312
 ED Entered STN: 20031105
 Last Updated on STN: 20031219
 Entered Medline: 20031211

AB We present a scheme for the classification of 3487 non-redundant protein structures into 1207 **non-hierarchical** clusters by using recurring structural patterns of three to six amino acids as keys of classification. This results in several signature patterns, which seem to decide membership of a protein in a functional category. The patterns provide clues to the key residues involved in functional sites as well as in protein-protein interaction. The discovered patterns include a "glutamate double bridge" of superoxide dismutase, the functional interface of the serine protease and inhibitor, interface of homo/hetero dimers, and functional sites of several enzyme families. We use geometric invariants to decide superimposability of structural patterns. This allows the parameterization of patterns and discovery of recurring patterns via **clustering**. The geometric invariant-based approach eliminates the computationally explosive step of pair-wise comparison of structures. The results provide a vast resource for the biologists for experimental validation of the proposed functional sites, and for the design of synthetic enzymes, inhibitors and drugs.

L4 ANSWER 4 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2004:205102 BIOSIS
 DN PREV200400205629
 TI Automated exploratory delineation and analysis of cortical areas.
 AU Eickhoff, S. [Reprint Author]; Schleicher, A.; Zilles, K. [Reprint Author]; Amunts, K. [Reprint Author]
 CS IME, Res. Ctr., Juelich, Germany
 SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2003) Vol. 2003, pp. Abstract No. 863.4. <http://sfn.scholarone.com>. e-file. Meeting Info.: 33rd Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 08-12, 2003. Society of Neuroscience.

DT Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
 LA English
 ED Entered STN: 14 Apr 2004
 Last Updated on STN: 14 Apr 2004

AB Observer-independent cytoarchitectonic mapping of the cerebral cortex(1,2) is based on the statistical analysis of its laminar pattern. This method reliably detects the position of areal borders by the identification of significant cytoarchitectonic changes. We here show an extension of this method, which enables an exploratory analysis of the laminar pattern in neighboring histological sections. Hereby, identical areas are identified automatically based on the measurement of cytoarchitectonic features. The GLI was measured as an indicator of the volume fraction of cell bodies. Profiles were obtained perpendicular to the cortical layers and their shape was quantified by 10 features(1). Architectonic borders were identified at those profiles-positions, where the multivariate Mahalanobis distance between neighboring groups of profiles showed local maxima(2). They were used to define the seeds for a **hierarchical** cluster analysis of the profiles within a section. A cut-off, representing the

most plausible number of groups, was calculated by evaluating a "penalty-function" based on the number of clusters and the introduced increase in variance. By applying a **non-hierarchical clustering**, the resulting classification of the profiles into areas was then used for recognizing identical areas on different sections. Results are in good accordance to those of visual inspection and established observer-independent methods(2). Our approach distinguishes reliably between cortical areas, as well as finer parcellations, e.g. within the extrastriate cortex. The approach automatically recognizes corresponding parts of the same cortical area in different sections and compensates for local variations and artifacts. This novel approach based on cluster analysis thus enables an automated, exploratory analysis of the cytoarchitecture in series of histological sections. 1 Schleicher et al, (1990) J Microsc 157:3672 Schleicher et al, (2000) J Chem Neuroanat 20:31.

L4 ANSWER 5 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:221538 BIOSIS
DN PREV200100221538

TI Comparison between modern **clustering** techniques and original macrobenthic community classification on A. Vatova's Adriatic data set (1934-36).

AU Di Dato, P. [Reprint author]; Fresi, E. [Reprint author]; Scardi, M.
CS Dipartimento di Biologia, Universita di Roma "Tor Vergata", Via della Ricerca Scientifica, 00133, Roma, Italy

SO Faranda, F. M.; Guglielmo, L.; Spezie, G. (2001) pp. 271-275.
Mediterranean ecosystems: Structures and processes. print.
Publisher: Springer-Verlag Italia Srl, Via Podgora 4, I-20122, Milan, Italy; Springer-Verlag New York Inc., 175 Fifth Avenue, New York, NY, 10010-7858, USA.
ISBN: 88-470-0114-5 (cloth).

DT Book
Book; (Book Chapter)

LA English

ED Entered STN: 9 May 2001
Last Updated on STN: 18 Feb 2002

L4 ANSWER 6 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:331507 BIOSIS
DN PREV200100331507

TI An avifaunal zonation of Switzerland and its relation to environmental conditions.

AU Pasinelli, Gilberto; Naef-Daenzer, Beat [Reprint author]; Schmid, Hans [Reprint author]; Keller, Verena [Reprint author]; Holzgang, Otto [Reprint author]; Graf, Roman [Reprint author]; Zbinden, Niklaus [Reprint author]
CS Swiss Ornithological Institute, 6204, Sempach, Switzerland
gpasi@vt.edu

SO Global Ecology and Biogeography, (May, 2001) Vol. 10, No. 3, pp. 261-274.
print.
ISSN: 1466-822X.

DT Article

LA English

ED Entered STN: 11 Jul 2001
Last Updated on STN: 19 Feb 2002

AB 1 We propose a quantitative zonation of Switzerland based on the distribution of breeding birds. We use a combined dataset from two

nationwide bird censuses 20 years apart to account for distribution changes between the censuses. This approach approximates the 'potential' distribution of species more closely than a dataset from one period only. 2 A numerical approach with correspondence analysis and **non-hierarchical clustering** resulted in five avifaunal regions, consisting of two lowland regions north of the alpine arch, two alpine regions and one region of southern alpine valleys. 3 We identified characteristic species for each region using the indicator value analysis of Dufrene and Legendre (1997) and determined environmental conditions separating the regions with discriminant analysis. 4 Our zonation partly corresponds with previous subdivisions of Switzerland, but has the advantage of being based on a numerical approach instead of expert knowledge. 5 We discuss avifaunal and ecological differences between the regions and relate our zonation to the classical biogeographic regions of Europe. Finally, we evaluate the importance of the zonation for bird conservation.

L4 ANSWER 7 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2001:185184 BIOSIS
 DN PREV200100185184
 TI Genetic divergence in seedling trees of Persian walnut (*Juglans regia* L.) for various metric nut and kernel characters in Himachal Pradesh.
 AU Sharma, O. C.; Sharma, S. D. [Reprint author]
 CS Department of Fruit Breeding and Genetic Resources, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, H.P., 173 230, India
 fbg@yspuhf.hp.nic.in
 SO Scientia Horticulturae (Amsterdam), (16 April, 2001) Vol. 88, No. 2, pp. 163-171. print.
 CODEN: SHRTAH. ISSN: 0304-4238.
 DT Article
 LA English
 ED Entered STN: 20 Apr 2001
 Last Updated on STN: 18 Feb 2002
 AB The nature and magnitude of genetic divergence was assessed using **non-hierarchical** Euclidean cluster analysis in 229 seedling trees of Persian walnut growing naturally in four districts of Himachal Pradesh for 15 nut and kernel characters. Minimum and maximum values of coefficients of variability were recorded for nut width and kernel weight, respectively. All genotypes were grouped into 16 different clusters. The **clustering** pattern of walnut genotypes belonging to the same location revealed their distribution in more than one cluster showing non-parallelism between geographic and genetic diversity. Genotypes of clusters 5 and 8 were highly diverse from each other. Mean nut weight and kernel weight were highest in clusters 8 and 14, respectively. The highest mean kernel percentage and minimum shell thickness were observed in cluster 13. The highest mean value for fat was recorded in cluster 9 whereas cluster 3 had the maximum value of protein.

L4 ANSWER 8 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2002:73354 BIOSIS
 DN PREV200200073354
 TI Analysis of variation in tissue culture response for identification of indica rice genotypes suitable for transformation.
 AU Visarada, K. B. R. S.; Kumar, C. H. M. Vijaya; Sarma, N. P. [Reprint author]

CS Directorate of Rice Research, Rajendranagar, Hyderabad, AP, 500 030, India
SO Journal of Genetics and Breeding, (June, 2001) Vol. 55, No. 2, pp.
125-134. print.
ISSN: 0394-9257.

DT Article
LA English
ED Entered STN: 16 Jan 2002
Last Updated on STN: 25 Feb 2002

AB Genetic variation for in vitro response of 22 elite indica rice cultivars along with Taipei-309, a japonica model variety for tissue culture studies, was investigated. Sequential growth stages of in vitro seed culture for example i) callus induction and regeneration ii) calli with green regions iii) calli with only shoots iv) calli with both roots and shoots v) calli with roots only and vi) plants per unit culture, were measured and analyzed by Duncan's multiple range test. The varieties were clustered into groups by taking into account all the in vitro growth stage parameters. **Clustering** of indica varieties by three methods viz., canonical analysis, joint score method and **non hierarchical** euclidean cluster analysis resulted in identification of 2,3 and 4 varieties respectively, in the same genetic cluster with Taipei-309. The analysis based on mean and standard deviation of joint scores for all the traits was shown to be superior to other two methods. Regeneration rather than callus induction was the limiting parameter in most of the varieties. The number of plants regenerated per unit culture and percent calli giving shoots was critical for any genotype before taking up transformation. The indica varieties Vibhava and Seshu were identified as close to Taipei-309 through genetic **clustering** and therefore should prove to be very suitable for transformation studies.

L4 ANSWER 9 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:206615 BIOSIS
DN PREV200100206615
TI High-resolution continuous soil classification using morphological soil profile descriptions.
AU Verheyen, Kris [Reprint author]; Adriaens, Dries; Hermy, Martin; Deckers, Seppe
CS Laboratory for Forest, Nature and Landscape Research, Catholic University of Leuven, V. Decosterstraat 102, B-3000, Leuven, Belgium
kris.verheyen@agr.kuleuven.ac.be
SO Geoderma, (April, 2001) Vol. 101, No. 3-4, pp. 31-48. print.
CODEN: GEDMAB. ISSN: 0016-7061.

DT Article
LA English
ED Entered STN: 25 Apr 2001
Last Updated on STN: 18 Feb 2002

AB Soil grid data were gathered from 156 points in the 30-ha Muizen forest (Ranst, Belgium). At each grid point, soil profiles were examined morphologically by augering to 120-cm depth. In the laboratory, pH(KCl) was determined on samples from every horizon. To allow numerical analyses, all the morphological attributes were given ordinal scores. The analysis consisted of two parts. First, the master horizons were split up into subtypes using Principal Components Analysis and a **non-hierarchical clustering** technique. This was necessary to overcome the problem of the anisotropy of the soil profiles, which makes it impossible to pool the data of all the horizons and analyse them together. Next, the distinguished horizon subtypes were used as input for

the continuous soil profile classification with the 'fuzzy k-means with extragrades' algorithm. Five different soil classes plus an extragrade class were distinguished. The distinguished soil classes exhibited a fair degree of spatial autocorrelation and correlated well with the Belgian Soil Map. The technique developed ensures the compatibility with national or global soil classification systems based on diagnostic horizons and properties on the one hand and the production of high-resolution soil classes for local use on the other. Furthermore, the developed technique allows reanalysis and optimisation of data from previous surveys.

L4 ANSWER 10 OF 35 MEDLINE on STN DUPLICATE 3
AN 2001196655 MEDLINE
DN PubMed ID: 11222259
TI PAQ: Partition Analysis of Quasispecies.
AU Baccam P; Thompson R J; Fedrigo O; Carpenter S; Cornette J L
CS Department of Mathematics, Iowa State University, Ames, IA 50011, USA..
pbaccam@lanl.gov
SO Bioinformatics (Oxford, England), (2001 Jan) 17 (1) 16-22.
Journal code: 9808944. ISSN: 1367-4803.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200105
ED Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010510
AB MOTIVATION: The complexities of genetic data may not be accurately described by any single analytical tool. Phylogenetic analysis is often used to study the genetic relationship among different sequences. Evolutionary models and assumptions are invoked to reconstruct trees that describe the phylogenetic relationship among sequences. Genetic databases are rapidly accumulating large amounts of sequences. Newly acquired sequences, which have not yet been characterized, may require preliminary genetic exploration in order to build models describing the evolutionary relationship among sequences. There are **clustering** techniques that rely less on models of evolution, and thus may provide nice exploratory tools for identifying genetic similarities. Some of the more commonly used **clustering** methods perform better when data can be grouped into mutually exclusive groups. Genetic data from viral quasispecies, which consist of closely related variants that differ by small changes, however, may best be partitioned by overlapping groups. RESULTS: We have developed an intuitive exploratory program, Partition Analysis of Quasispecies (PAQ), which utilizes a **non-hierarchical** technique to partition sequences that are genetically similar. PAQ was used to analyze a data set of human immunodeficiency virus type 1 (HIV-1) envelope sequences isolated from different regions of the brain and another data set consisting of the equine infectious anemia virus (EIAV) regulatory gene rev. Analysis of the HIV-1 data set by PAQ was consistent with phylogenetic analysis of the same data, and the EIAV rev variants were partitioned into two overlapping groups. PAQ provides an additional tool which can be used to glean information from genetic data and can be used in conjunction with other tools to study genetic similarities and genetic evolution of viral quasispecies.

L4 ANSWER 11 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 2001:279111 BIOSIS
 DN PREV200100279111
 TI Introduction to the exploration of multivariate biological data.
 AU Podani, Janos [Reprint author]
 CS L. Eotvos University, Budapest, Hungary
 SO Podani, Janos. (2000) pp. i-vi, 1-407. Introduction to the exploration of multivariate biological data. print.
 Publisher: Backhuys Publishers, P. O. Box 321, 2300 AH, Leiden, Netherlands.
 ISBN: 90-5782-067-6 (paper).
 DT Book
 LA English
 ED Entered STN: 13 Jun 2001
 Last Updated on STN: 19 Feb 2002
 AB This book collects the major aspects of applying multivariate analysis to general biological problems. The chapters illustrate a large diversity of biological topics to illuminate as many approaches to data exploration as possible. Selected software packages that facilitate analysis are discussed. The book includes bibliographical references and a subject index.

L4 ANSWER 12 OF 35 MEDLINE on STN
 AN 2001127964 MEDLINE
 DN PubMed ID: 11097075
 TI An empirical approach to subtype identification in individuals with social phobia.
 AU Eng W; Heimberg R G; Coles M E; Schneier F R; Liebowitz M R
 CS Adult Anxiety Clinic, Temple University, Philadelphia, PA, USA.
 NC MH40121 (NIMH)
 MH44119 (NIMH)
 MH47831 (NIMH)
 +
 SO Psychological medicine, (2000 Nov) 30 (6) 1345-57.
 Journal code: 1254142. ISSN: 0033-2917.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 200102
 ED Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20010222
 AB BACKGROUND: The present study used cluster analysis procedures to identify empirically subgroups of patients with social phobia in a large clinical sample. METHOD: The Liebowitz Social Anxiety Scale (LSAS) was administered to 382 patients from several studies of the treatment of social phobia. LSAS fear ratings were summed into four subscale scores (social interaction, public speaking, observation by others, eating and drinking in public) based on a previous factor analytical study of the LSAS. In order to produce a stable and robust solution, these factor scores were submitted to a two-stage **clustering** procedure consisting of an agglomerative-**hierarchical clustering** method followed by an iterative **non-hierarchical clustering** method. RESULTS: Three patient subgroups were identified based on their pattern of feared social situations on the LSAS. These groups were labelled: (1) pervasive social anxiety; (2) moderate

social interaction anxiety; and (3) dominant public speaking anxiety. Clusters differed significantly on age and age of social phobia onset, as well as on measures of social anxiety, general anxiety and depressive symptomatology. Clusters also differed in the percentage of assigned patients who met criteria for the generalized subtype of social phobia and avoidant personality disorder. CONCLUSIONS: The results provide empirical support for the existence of three subgroups in a clinical sample of individuals with social phobia and contribute to the growing evidence for the heterogeneity of social phobia. Further study of the conceptual, clinical and aetiological significance of these subgroups is needed.

L4 ANSWER 13 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2000:120537 BIOSIS
 DN PREV200000120537
 TI Attribute-based classification of European hydrophytes and its relationship to habitat utilization.
 AU Willby, Nigel J. [Reprint author]; Abernethy, Vicky J.; Demars, Benoit O. L.
 CS Department of Environmental Science, University of Stirling, Stirling, FK9 4LA, UK
 SO Freshwater Biology, (Jan., 2000) Vol. 43, No. 1, pp. 43-74. print. CODEN: FWBLAB. ISSN: 0046-5070.
 DT Article
 LA English
 ED Entered STN: 29 Mar 2000
 Last Updated on STN: 3 Jan 2002
 AB 1. Here we classify selected European hydrophytes into 'attribute groups' based on the possession of homogenous sets of characteristics, and explore the correspondence between these attribute groups, or individual attributes, and habitat use. 2. **Non-hierarchical clustering** was used to assign 120 species to twenty groups based on a matrix of categorical scores for literature- and field-derived information covering seventeen intrinsic morphological and life-history traits. Subdivision of some of these traits produced a total of 58 attributes (i.e. modalities). The robustness of this classification was confirmed by a high rate of reclassification (92%) under multiple discriminant analysis (MDA). The phylogenetic contribution was explored using ordination methods with taxonomy at family level acting as a covariable. 3. Our approach differed from earlier classifications based on growth or life form because we regarded growth form plasticity as a property of the species and its range of growing conditions, rather than of each individual population, and we considered additional (e.g. regenerative) traits. However, some conventional life form groups were preserved (i.e. utricularids, isoetids, hydrocharids and lemoids). 4. Some parallels existed with established theory on terrestrial plant growth strategies, but we used strictly intrinsic attributes relevant specifically to hydrophytes and our groups could not be decomposed into three or four primary strategies. Only finer levels of partitioning appear to be of fundamental and applied ecological relevance in hydrophytes. 5. A principal components analysis ordination based on 26 attributes related to physical habitat utilization separated species and their attribute groups along axes relating to: (a) flow, substratum grade and organic matter content, scour frequency, and sedimentation; and (b) depth, water level stability and biotic disturbance. A MDA applied to species ordination scores indicated only a modest overall correspondence between attribute groups and habitat use (54% correct reclassification).

Poor reclassification was the result of intergroup overlap (indicating alternative sets of attributes for a given habitat) or high intragroup variance in habitat utilization (indicating commonality of attributes between different habitats). These results are interpreted in terms of trade-offs between resistance and resilience traits, 'functional plasticity' in traits, phylogenetic dependence in some groups and methodological constraints. The predictive potential of hydrophyte groups and their limitations are discussed. 6. Redundancy analysis revealed a highly significant correlation between traits and habitat use ($P < 0.01$). Our attribute matrix explained 72% of variation in physical habitat use with eight attributes (i.e. turions, anchored emergent leaves, high or low body flexibility, high root:shoot biomass ratio, free-floating surface or free-floating submerged growth form, and annual life history) explaining half of this variation. 7. Most attributes were mapped in accordance with habitat template predictions, although tests were confounded by the underlying correlation between spatial and temporal heterogeneity. The main features were: (a) a trade-off between resistance-type traits (related to stream lining, flexibility and anchorage) in more spatially heterogeneous riverine and littoral zone habitats, and resilience type traits (i.e. turions, very small body size and free-floating growth forms) in spatially simple, rarely disturbed habitats, such as backwaters and canals; and (b) a shift from high investment competitive traits with a low reproductive output in deep stable habitats to classically ruderal and desiccation resistance traits in shallow fluctuating habitats.

L4 ANSWER 14 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1999:253766 BIOSIS
 DN PREV199900253766
 TI Use of cluster analysis to validate IHS diagnostic criteria for migraine and tension-type headache.
 AU Bruehl, Stephen [Reprint author]; Lofland, Kenneth R.; Semenchuk, Elizabeth M.; Rokicki, Lori A.; Penzien, Donald B.
 CS Center for Pain Studies, Rehabilitation Institute of Chicago, 345 East Superior Street, Room 904, Chicago, IL, 60611, USA
 SO Headache, (March, 1999) Vol. 39, No. 3, pp. 181-189. print.
 CODEN: HEADAE. ISSN: 0017-8748.
 DT Article
 LA English
 ED Entered STN: 2 Jul 1999
 Last Updated on STN: 2 Jul 1999
 AB Cluster analysis was used to validate headache diagnostic criteria of the International Headache Society (IHS). Structured diagnostic interviews were conducted on 443 headache sufferers from a community sample, which was randomly split to allow replication. **Hierarchical** cluster analysis of symptoms in both subsamples revealed two distinct ($P < .001$) clusters: (1) unilateral pulsating pain, pain aggravated by activity, and photophobia and phonophobia, and (2) bilateral pressing/tightening pain, mild to moderate intensity, and absence of nausea/vomiting. These clusters were consistent with IHS migraine and tension-type classifications, respectively. Replication using a **non-hierarchical clustering** technique, k-means cluster analysis, revealed a migrainelike patient cluster, reflecting more frequent pulsating, unilateral pain; more severe pain; and pain aggravated by activity; nausea, vomiting, photophobia, and phonophobia. A tensionlike patient cluster was also identified, reflecting more frequent pressing/tightening pain, mild to moderate pain, bilateral location, and

absence of nausea/vomiting. These patient clusters were consistent across subsamples. International Headache Society diagnoses corresponded with classification based upon statistically derived clusters ($P < .001$). These results indicate that headache symptoms cluster empirically in a manner consistent with IHS criteria for migraine and tension-type headaches. Criterion overlap problems regarding pain intensity and duration were identified. Overall, these data support migraine and tension-type headache as distinct entities, and provide support for the IHS diagnostic criteria with minor modifications.

L4 ANSWER 15 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:238053 BIOSIS
DN PREV199900238053
TI Classification and receptor modeling of wet precipitation data from Central Austria (1984-1993).
AU Simeonov, V. [Reprint author]; Puxbaum, H.; Tsakovski, S.; Sarbu, C.; Kalina, M.
CS Faculty of Chemistry, University of Sofia 'St. Kliment Okhridski', J. Bourchier Blvd. 1, 1126, Sofia, Bulgaria
SO Environmetrics, (March-April, 1999) Vol. 10, No. 2, pp. 137-152. print. ISSN: 1180-4009.
DT Article
LA English
ED Entered STN: 17 Jun 1999
Last Updated on STN: 17 Jun 1999
AB Various classification procedures (**hierarchical** and **non-hierarchical** crisp and fuzzy **clustering**, cross-classification fuzzy **clustering**) and principal component analysis (varimax rotation) combined with receptor modeling are applied to a data set consisting of wet deposition loads of major ions from five sampling sites in Central Austria collected in a period of 10 years (1984-1993). The data classification with respect to the sampling sites as objects has shown that a distinct separation between sites located at the northern Alpine rim (Reutte, Kufstein and Haunsberg) and in the inner Alpine region (Innervillgraten and Werfenweng) is achieved indicating in this way the role of the geographical disposition of the sampling sites. Both cluster and principal components analysis proved that three conditional (latent) factors are responsible for the data structure called in this study 'anthropogenic', 'crustal' and 'mixed salt' - (NH_4^+ , SO_4^{2-} , NO_3^- , H^+), (Ca^{2+} , Mg^{2+}), (K^+ , Na^+ , Cl^-), respectively. The source apportioning model has indicated that anthropogenic gaseous emissions might be responsible for the first factor, natural crustal influences and Sahara events for the second and sea salt and manure for the third.

L4 ANSWER 16 OF 35 MEDLINE on STN
AN 1998178077 MEDLINE
DN PubMed ID: 9517009
TI An evaluation of structural descriptors and **clustering** methods for use in diversity selection.
AU Brown R D; Martin Y C
CS Pharmaceutical Products Division, Abbott Laboratories, Abbott Park, IL 60064-350, USA.
SO SAR and QSAR in environmental research, (1998) 8 (1-2) 23-39. Journal code: 9440156. ISSN: 1062-936X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)

LA English
 FS Priority Journals
 EM 199804
 ED Entered STN: 19980507
 Last Updated on STN: 19980507
 Entered Medline: 19980429

AB An evaluation of the suitability of a number of structural descriptors and **clustering** methods for use in diversity selection is presented. The methods are compared by their success in simulated biological activity predictions. The results suggest that simple 2D structural descriptors are particularly effective and that **hierarchical clustering** methods are superior to the **non-hierarchical** methods traditionally used for diversity related tasks. Results are presented which suggest that the difference in the utility of the descriptors can be accounted for by the different extent to which each encodes information relevant to the forces of ligand-receptor binding.

L4 ANSWER 17 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1998:223350 BIOSIS
 DN PREV199800223350
 TI Hybrids and phylogenetic systematics III. Comparison with distance methods.
 AU McDade, Lucinda A. [Reprint author]
 CS Dep. Ecol. Evolutionary Biol., Plant Sci., Univ. Arizona, Tucson, AZ 85721, USA
 SO Systematic Botany, (Oct.-Dec., 1997) Vol. 22, No. 4, pp. 669-683. print. CODEN: SYBODA. ISSN: 0363-6445.
 DT Article
 LA English
 ED Entered STN: 20 May 1998
 Last Updated on STN: 20 May 1998

AB Three distance methods including two **hierarchical clustering** methods (average linkage (UPGMA) and Neighbor joining, NJ) and one **non-hierarchical** ordination method (Multidimensional Scaling, MDS) were used to analyze data sets including taxa of known hybrid origin and their parents. Whereas goodness of fit measures indicated reduced success of MDS and parsimony analyses with increasing numbers of hybrids, neither UPGMA nor NJ analyses were affected by number of hybrids. Compared to analyses with the same number of taxa, all of which were species, goodness of fit measures indicated that all analytic methods had more difficulty handling species than hybrids. These measures are unlikely, therefore, to provide any signal of the presence of hybrids. Results were also compared in terms of placement of hybrids relative to parents and other taxa. UPGMA (and raw distance values) reliably placed many hybrids closest to one or both parents. In contrast, NJ placed hybrids in the same manner as parsimony: usually as the basal member of a lineage including one or both parents along with other taxa. These results support the idea that NJ yields topologies that are similar to explicit phylogenetic methods. However, in the special case of hybrids, these topologies, in parallel with those from parsimony analyses, provide no indication of the presence or special evolutionary history of hybrids. If identification of hybrids is the goal, these results suggest that pairwise distances are more useful than any of the methods explored.

L4 ANSWER 18 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1998:91345 BIOSIS
 DN PREV199800091345
 TI Vegetation on hill slopes in southern Wello, Ethiopia: Degradation and regeneration.
 AU Tekle, Kebrom [Reprint author]; Backeus, I.; Skoglund, J.; Woldu, Zerihun
 CS Dep. Ecological Botany, Uppsala Univ., Villavagen 14, S-752 36 Uppsala, Sweden
 SO Nordic Journal of Botany, (1997) Vol. 17, No. 5, pp. 483-493. print.
 CODEN: NJBODK. ISSN: 0107-055X.
 DT Article
 LA English
 ED Entered STN: 25 Feb 1998
 Last Updated on STN: 25 Feb 1998
 AB A study was made of the vegetation in southern Wello (Ethiopia) in relation to human impact and the environment. 65 sample plots were laid out and analysed with respect to the cover value of vascular plant species. Altitude, slope, aspect and estimates of grazing pressure for each plot were also recorded along with physical and chemical soil properties analysed for samples taken from each plot. The following environmental factors, isolated by forward selection, show correlation with the axes of Canonical Correspondence Analysis (CCA): altitude, grazing, pH, K, Ca, Mg, slope and aspect. Through **hierarchical** and **non-hierarchical clustering** methods the vegetation was divided into eight types, from which one was secondary forest characterised by patch dominance of *Juniperus procera* and *Olea europaea* ssp. *cuspidata*. These forest patches are found at high altitude sites and because of their inaccessibility are usually characterised by low livestock density and consequently low grazing pressure. The presence of large boulders and stones in *Podocarpus falcatus* forest decreases accessibility and creates natural protection for the trees. The other vegetation types, most of which are found at lower altitude and associated with varying intensities of grazing, include grasslands (grazed and protected), regenerating sites dominated by *Euclea racemosa* and *Dodonaea angustifolia*, dense and open shrublands and *Olea europaea* ssp. *cuspidata* woodlands. Human interference has a major impact on the vegetation of the study area and its recovery will depend on the degree of participation of the local people.

L4 ANSWER 19 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1997:339158 BIOSIS
 DN PREV199799638361
 TI The analysis of large scale data taken from the world groundnut (*Arachis hypogaea* L.) germplasm collection: I. Two-way quantitative data.
 AU Harch, B. D. [Reprint author]; Basford, K. E.; Delacy, I. H.; Lawrence, P. K.
 CS CSIRO, Math. Inf. Sci., PMB 2, Glen Osmond, SA 5064, Australia
 SO Euphytica, (1997) Vol. 95, No. 1, pp. 27-38.
 CODEN: EUPHAA. ISSN: 0014-2336.
 DT Article
 LA English
 ED Entered STN: 11 Aug 1997
 Last Updated on STN: 11 Aug 1997
 AB Data associated with germplasm collections are typically large and multivariate with a considerable number of descriptors measured on each of many accessions. Pattern analysis methods of **clustering** and ordination have been identified as techniques for statistically evaluating

the available diversity in germplasm data. While used in many studies, the approaches have not dealt explicitly with the computational consequences of large data sets (i.e. greater than 5000 accessions). To consider the application of these techniques to germplasm evaluation data, 11328 accessions of groundnut (*Arachis hypogaea* L) from the International Research Institute for the Semi-Arid Tropics, Andhra Pradesh, India were examined. Data for nine quantitative descriptors measured in the rainy and post-rainy growing seasons were used. The ordination technique of principal component analysis was used to reduce the dimensionality of the germplasm data. The identification of phenotypically similar groups of accessions within large scale data via the computationally intensive **hierarchical clustering** techniques was not feasible and **non-hierarchical** techniques had to be used. Finite mixture models that maximise the likelihood of an accession belonging to a cluster were used to cluster the accessions in this collection. The patterns of response for the different growing seasons were found to be highly correlated. However, in relating the results to passport and other characterisation and evaluation descriptors, the observed patterns did not appear to be related to taxonomy or any other well known characteristics of groundnut.

- L4 ANSWER 20 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1997:198429 BIOSIS
 DN PREV199799497632
 TI Evaluation of genetic divergence in wheat (*Triticum aestivum* L.)
 germplasm.
 AU Walia, D. P. [Reprint author]; Garg, D. K.
 CS Dep. Fruit Breeding, Univ. Horticulture Forestry, Nauni, Solan 173 230,
 India
 SO Indian Journal of Genetics and Plant Breeding, (1996) Vol. 56, No. 4, pp.
 452-457.
 CODEN: IJGBAG. ISSN: 0019-5200.
 DT Article
 LA English
 ED Entered STN: 12 May 1997
 Last Updated on STN: 12 May 1997
 AB The nature and magnitude of genetic diversity was assessed using
non-hierarchical euclidean cluster analysis in 405 pure
 breeding lines of *T. aestivum* for grain yield and its associated traits.
 All the genotypes got grouped in 13 different clusters. The
clustering pattern of the genotypes belonging to the same country
 revealed their distribution in more than one cluster showing
 nonparallelism between geographic and genetic diversity. Members of
 cluster IV and IX were highly diverse from each other. Cluster VI had
 high mean values for grain yield, biological yield, number of tillers/unit
 area and harvest index. A number of genotypes were also identified which
 may serve as potent genetic donors for some metric traits.
- L4 ANSWER 21 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1996:573845 BIOSIS
 DN PREV199799288526
 TI Floristic patterns and phytogeography of Skane, S Sweden.
 AU Andersson, Per-Arne [Reprint author]; Weimarck, Gunnar
 CS Dep. Ecological Botany, Villavagen 14, S-752 36 Uppsala, Sweden
 SO Acta Universitatis Upsaliensis Symbolae Botanicae Upsalienses, (1996) Vol.
 31, No. 3, pp. 239-264.

CODEN: SBUPAC. ISSN: 0082-0644.

DT Article

LA English

ED Entered STN: 23 Dec 1996

Last Updated on STN: 23 Dec 1996

AB Dot maps of the distribution of 895 vascular plant taxa in the province of Skane, S Sweden, were digitized and the records assigned to 483 quadrats of 5 times 5 km each. Quadrats and species were classified by the **non-hierarchical** agglomerative **clustering** program TABORD and ordinated by the program DECORANA. The results are given in a phytosociological table and as grid map plots and ordination graphs. Gradients are interpreted and clusters described in terms of Ellenberg's indicator scores. A regional floristic subdivision of the province in eight areas is proposed. The position of the border, 'limes scanicus', between two previously proposed major areas is modified here.

L4 ANSWER 22 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1996:43753 BIOSIS

DN PREV199698615888

TI Ecological Computations Series, Volume 6. Multivariate data analysis in ecology and systematics: A methodological guide to the SYN-TAX 5.0 package.

AU Podani, Janos

CS Dep. Plant Ecol. Taxon., L. Eotvos Univ., Ludovika ter 2, H-1083 Budapest, Hungary

SO Podani, J. (1994) pp. 316p. Ecological Computations Series; Multivariate data analysis in ecology and systematics: A methodological guide to the SYN-TAX 5.0 package.

Publisher: SPB Academic Publishing bv, PO Box 97747, 2509 GC Amsterdam, Netherlands. Series: Ecological Computations Series.

ISBN: 90-5103-094-0.

DT Book

Software Review

LA English

ED Entered STN: 2 Feb 1996

Last Updated on STN: 2 Feb 1996

AB This book is a guide to the SYN-TAX 5.0 programs. SYN-TAX 5.0 is a package of over 50 programs designed for multivariate statistical analyses in ecological and statistical studies. The programs operate under DOS and may be initiated from Windows. The book describes the use of SYN-TAX in **non-hierarchical** and **hierarchical clustering**, ordination and matrix rearrangement, comparisons, consensus techniques, Monte Carlo simulations, and analysis of multispecies point patterns. A glossary, references, and a subject index are included, and the text is illustrated with graphs, charts, mathematical formulae, and tables.

L4 ANSWER 23 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1994:526576 BIOSIS

DN PREV199497539576

TI Computer-assisted mapping of paddy-field soils: II. Classification, mapping and significance.

AU Ishida, Tomoyuki [Reprint author]; Ando, Ho

CS Fac. Agric., Kagawa Univ., Kida-gun, Kagawa 761-07, Japan

SO Soil Science and Plant Nutrition, (1994) Vol. 40, No. 3, pp. 403-414.

CODEN: SSPNAW. ISSN: 0038-0768.

DT Article
 LA English
 ED Entered STN: 15 Dec 1994
 Last Updated on STN: 16 Dec 1994

AB In order to determine how a conventional soil map on a local scale can be reproduced from soil sample information, a set of numerical procedures was applied to the soil chemical data from 159 soil samples collected in paddy fields of the Aizu Basin, in the northern part of Japan. The digital elevation data were also included as an attribute. Various steps were involved. In the first step, the sparse data were converted into a closely spaced data set. This first step was previously described in Part I of this paper. In the second step a multivariate ordination (principal component analysis) was applied to the sampling data in order to avoid redundancy of information. Large contributions to the first component were derived from the values of CEC and exchangeable Ca and Mg. In the third step the sampling sites were numerically classified using the results of four or five components obtained in the second step. A **hierarchical clustering** method was applied to provide the initial set of clusters for **non-hierarchical clustering**. In the fourth step the closely spaced data collected in the first step were allocated to an appropriate class obtained by using the **non-hierarchical clustering** method applied in the third step. For the allocation method, the geographic location of the sampling sites was included as an additional characteristic of the data. In the regional partition map based on the numerical procedures, each soil group corresponded to a soil series in the original conventional soil map which depended predominantly on detailed morphological and topographical differences. In addition, the regional partition map was found to provide useful information for the identification of factors closely related to soil fertility, by statistically examining the differences in rice yield among the soil groups.

L4 ANSWER 24 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1993:386396 BIOSIS
 DN PREV199396061696
 TI Comparing three classification strategies for use in ecology.
 AU Belbin, Lee [Reprint author]; McDonald, Cam
 CS CSIRO Div. Wildlife and Ecol., PO Box 84, Lyneham, ACT Australia 2602, australia
 SO Journal of Vegetation Science, (1993) Vol. 4, No. 3, pp. 341-348.
 CODEN: JVESEK. ISSN: 1100-9233.

DT Article
 LA English
 ED Entered STN: 23 Aug 1993
 Last Updated on STN: 23 Aug 1993

AB We compare three common types of **clustering** algorithms for use with community data. TWINSpan is divisive **hierarchical**, flexible-UPGMA is agglomerative and **hierarchical**, and ALOC is **non-hierarchical**. A balanced design six-factor model was used to generate 480 data sets of known characteristics. Recovery of the embedded clusters suggests that both flexible UPGMA and ALOC are significantly better than TWINSpan. No significant difference existed between flexible UPGMA and ALOC.

L4 ANSWER 25 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1992:522932 BIOSIS
 DN PREV199294131007; BA94:131007
 TI DIFFERENTIATION AND GROUPING CHARACTERISTICS OF VARIETAL GRAPE MUSTS AND
 WINES FROM MAJORCAN ORIGIN.
 AU MULET A [Reprint author]; BERNA A; FORCEN M
 CS DEP FOOD TECHNOL, UNIV POLITECNICA VALENCIA, CAMINO VERA 14, 46071
 VALENCIA, SPAIN
 SO American Journal of Enology and Viticulture, (1992) Vol. 43, No. 3, pp.
 221-226.
 CODEN: AJEVAC. ISSN: 0002-9254.
 DT Article
 FS BA
 LA ENGLISH
 ED Entered STN: 19 Nov 1992
 Last Updated on STN: 20 Nov 1992
 AB Forty-six samples of three Majorcan red grape musts, Manto Negro, Callet,
 and Fogoneu, from two close viticultural regions, Zona Alta and Zona Baja,
 were tested on the basis of twelve conventional variables.
 Physicochemical data were treated by pattern recognition techniques by
 means of discriminant analysis and **non-hierarchical**
clustering, thus allowing characterization according to the
 geographical and varietal origin of samples. Discriminant analysis gave
 rise to coincident classification results (average percentage error 18.5%)
 when distinguishing both varieties and zones. **Clustering**
 analysis revealed a strong varietal affinity among the studied grape
 samples. A further comparative study for the musts considered and the
 corresponding wines, previously studied for sixteen conventional
 variables, showed that in the discriminant statistical treatment
 correlation could be established among cultivars in terms of color
 intensity and nitrogen content. Musts and wines from different zones were
 fairly related to some geographical characteristics of the regions. When
 considering **hierarchical clustering**, an evident
 relationship between musts and wines was exclusively achieved by means of
 the varietal origin of the samples.

L4 ANSWER 26 OF 35 MEDLINE on STN
 AN 94084457 MEDLINE
 DN PubMed ID: 1341650
 TI Cluster analysis and related techniques in medical research.
 AU McLachlan G J
 CS Department of Mathematics, University of Queensland, Australia.
 SO Statistical methods in medical research, (1992) 1 (1) 27-48. Ref: 54
 Journal code: 9212457. ISSN: 0962-2802.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, ACADEMIC)
 LA English
 FS Priority Journals
 EM 199401
 ED Entered STN: 19940209
 Last Updated on STN: 19990129
 Entered Medline: 19940127
 AB In this paper we review methods of cluster analysis in the context of
 classifying patients on the basis of clinical and/or laboratory type
 observations. Both **hierarchical** and **non-**

hierarchical methods of **clustering** are considered, although the emphasis is on the latter type, with particular attention devoted to the mixture likelihood-based approach. For the purposes of dividing a given data set into *g* clusters, this approach fits a mixture model of *g* components, using the method of maximum likelihood. It thus provides a sound statistical basis for **clustering**. The important but difficult question of how many clusters are there in the data can be addressed within the framework of standard statistical theory, although theoretical and computational difficulties still remain. Two case studies, involving the cluster analysis of some haemophilia and diabetes data respectively, are reported to demonstrate the mixture likelihood-based approach to **clustering**.

L4 ANSWER 27 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1989:355631 BIOSIS
 DN PREV198988047745; BA88:47745
 TI MIDWATER FOOD WEB IN THE VICINITY OF A MARGINAL ICE ZONE IN THE WESTERN
 WEDDELL SEA ANTARCTIC.
 AU HOPKINS T L [Reprint author]; TORRES J J
 CS DEP MARINE SCI, UNIV SOUTH FLORIDA, 140 7TH AVE SOUTH, ST PETERSBURG, FLA
 33701, USA
 SO Deep-Sea Research Part A Oceanographic Research Papers, (1989) Vol. 36,
 No. 4, pp. 543-560.
 CODEN: DRPPD5. ISSN: 0198-0149.
 DT Article
 FS BA
 LA ENGLISH
 ED Entered STN: 2 Aug 1989
 Last Updated on STN: 2 Aug 1989
 AB The structure of the food web in the vicinity of a marginal ice zone was
 investigated in the western Weddell Sea during austral autumn 1986. The
 diets of 40 species of zooplankton and micronekton occurring in the
 epipelagic zone were examined and compared using **non-**
hierarchical clustering procedures. Over half the
 species were in three clusters of predominately small-particle
 (phytoplankton; protozoans) grazers. These included biomass dominants
 Calanoides acutus, Calanus propinquus, Metridia gerlachei and Salpa
 thompsoni. Six clusters contained omnivores that had diets consisting of
 small particles as well as a substantial fraction of metazoan food. Among
 these was Euphausia superba. Seven groups were carnivorous, including
 species of copepods (1), chaetognaths (3), and fishes (5). Copepods were
 the most frequent food of carnivores; however krill also were important in
 the diets of three fish species. Among small-particle grazers,
 phytoplankton occurred more frequently in guts in individuals from open
 water; carnivory was more in evidence in samples collected under the pack
 ice. Regional comparisons of material taken on this and several previous
 cruises indicate that, in most of the dominant species, diets remain
 relatively consistent with respect to major food categories. Seasonal
 impact on feeding dynamics appears to be great: the guts of grazing
 species were generally much more full (visual evidence) during summer
 bloom conditions than during the autumn. The following trophic sequence
 is suggested for grazing zooplankton species in ice-covered regions of the
 Antarctic: (1) Active small-particle grazing during the summer bloom
 period; (2) reduced ingestion rates in autumn as primary production
 declines and the system becomes more oligotrophic, with some species
 augmenting grazing with carnivory; (3) descent of zooplankton biomass

species into the mesopelagic zone in late autumn-early winter with feeding largely terminated. The sequence applies to the dominant zooplankton biomass species. Feeding dynamics and vertical distribution of several of the important larger sized grazing species, such as Euphausia superba and Salpa thompsoni, remain largely unknown.

L4 ANSWER 28 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1990:223971 BIOSIS
DN PREV199089121261; BA89:121261
TI MULTIVARIATE APPROACH TO GROUPING SOILS IN SMALL FIELDS II. SOIL GROUPING
TECHNIQUE BY CLUSTER ANALYSIS.
AU KOSAKI T [Reprint author]; JUO A S R
CS DEP AGRO-ENVIRON SCI, OBIHIRO UNIV AGRIC VETERINARY MED, OBIHIRO 080, JPN
SO Soil Science and Plant Nutrition, (1989) Vol. 35, No. 4, pp. 517-526.
CODEN: SSPNAW. ISSN: 0038-0768.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 10 May 1990
Last Updated on STN: 10 May 1990
AB Cluster analysis was applied in grouping soils based on their scores of
the factors controlling soil variation in a cultivated, field at the
Experimental Farm of the International Institute of Tropical Agriculture in
Ibadan, Nigeria. The procedure employed here consisted of two steps: 1)
grouping of the samples into a given number of provisional clusters
through **non-hierarchical** cluster analysis, and 2)
analysis of the similarity among those clusters using their means with
hierarchical cluster analysis and determination of the proper
number of the final clusters. Two initial settings in the assignment of
the number of the provisional clusters were tested in **non-**
hierarchical cluster analysis. Both trials gave a consistent
classification, which also agreed with that based only on
hierarchical cluster analysis. This combination of **non-**
hierarchical and **hierarchical** cluster analyses enabled
us to pressure a soil map solely based on the factors controlling soil
variation in the study area without introducing an a priori idea of soil
classification. This method is not only an alternative to
hierarchical clustering, but a more efficient tool in
terms of capacity and computational speed to classify large numbers of
samples which **hierarchical** cluster analysis is unable to handle.

L4 ANSWER 29 OF 35 MEDLINE on STN
AN 87149250 MEDLINE
DN PubMed ID: 3493535
TI Mental disorders and ecological structure in Nottingham.
AU Giggs J A
SO Social science & medicine (1982), (1986) 23 (10) 945-61.
Journal code: 8303205. ISSN: 0277-9536.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198703
ED Entered STN: 19900303
Last Updated on STN: 19900303
Entered Medline: 19870330

AB This paper presents the findings of a specifically geographical investigation of the incidence, distribution and social/environmental correlates of mental disorder in Nottingham. Three diagnostic groups were examined, namely schizophrenia and paranoia, the effective psychoses (or manic depression) and the non-psychotic mental disorders. Analysis of two distinct cohorts of first contact patients for both the schizophrenia and affective psychoses diagnoses yielded markedly dissimilar incidence rates. It is therefore suggested that observed variations in the incidence of specific mental disorders between cities probably reflect such nosocomial (i.e. service related) factors as diagnostic accuracy and the levels of local psychiatric services. It is therefore dangerous to ascribe the variations solely to the contrasting social/environmental milieux found in these cities. The spatial distributions of the selected mental disorders within Nottingham were analysed in the context of a set of 12 distinct ecological areas. These areas were derived from a matrix comprising 105 sub-areas and 40 variables via principal components analysis and a **non-hierarchical clustering** algorithm. Marked spatial variation in the incidence of all the mental disorders was demonstrated via both traditional mapping and probability mapping techniques. Pearson product-moment analysis revealed that the distributions of the two diagnostically distinct schizophrenia and affective psychoses cohorts were virtually identical. The relationships between the inception rates for the mental disorders and social/environmental attributes were analysed. Stepwise multiple regression models for both the principal components and the individual census variables revealed strong and systematic relationships with all the mental disorders. Although such ecological analysis has limited explanatory power it nevertheless provides useful insights into mental disorder-environmental relationships. It is argued that these can be subsequently best examined at a disaggregated (i.e. behavioural) level.

L4 ANSWER 30 OF 35 MEDLINE on STN DUPLICATE 4
AN 86018819 MEDLINE
DN PubMed ID: 4048928
TI Heterotrophic bacteria in water distribution systems. I. Spatial and temporal variation.
AU Maul A; el-Shaarawi A H; Block J C
SO Science of the total environment, (1985 Sep) 44 (3) 201-14.
Journal code: 0330500. ISSN: 0048-9697.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198511
ED Entered STN: 19900321
Last Updated on STN: 19900321
Entered Medline: 19851114

AB The drinking water distribution system of the city of Metz in France was sampled intensively during six, monthly surveys which were designed to determine the spatial and temporal distribution of total heterotrophic bacteria in the network. A **non-hierarchical** nearest-centroid **clustering** method was used for dividing the water distribution system into zones corresponding to different levels of bacterial density. The general pattern of the spatial heterogeneity showed a high degree of reproducibility. Since the frequency distribution of total heterotrophic bacteria within the zones was compatible with the

negative binomial distribution, the water distribution system studied may be considered as being composed of several heterogeneous subsystems. The consistency of this structured spatial dispersion pattern of bacteria in light of some physical and chemical characteristics of the system is evident. In consideration of the principal features of flow in the system relevant to the layout of water mains, the location of zones of highest bacterial concentrations have been attributed to lower levels of chlorine residuals and prolonged retention time of the water in the network, especially in the storage units, before reaching the various distribution areas. Although the monthly variation in the bacterial concentration of the entire system showed a marked increase which was concomitant with warmest water temperatures, the zones were subject to noticeable discrepancies in the range of temporal variation.

L4 ANSWER 31 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1984:337831 BIOSIS
 DN PREV198478074311; BA78:74311
 TI DISSOLVED OXYGEN CONCENTRATIONS IN LAKE ERIE USA CANADA 1. STUDY OF
 SPATIAL AND TEMPORAL VARIABILITY USING CLUSTER AND REGRESSION ANALYSIS.
 AU ANDERSON J E [Reprint author]; EL-SHAARAWI A H; ESTERBY S R; UNNY T E
 CS DEP OF CIVIL ENGINEERING, UNIV OF WATERLOO, WATERLOO, ONT N2L 3G1, CANADA
 SO Journal of Hydrology (Amsterdam), (1984) Vol. 72, No. 3-4, pp. 209-230.
 CODEN: JHYDA7. ISSN: 0022-1694.
 DT Article
 FS BA
 LA ENGLISH
 AB **A non-hierarchical** nearest-centroid **clustering**
 method was used to separate data pairs consisting of the dissolved oxygen
 (DO) concentration and temperature into 4 groups corresponding to
 hypolimnetic and non-hypolimnetic water of the Central and Eastern Basins
 of Lake Erie. For the stations which were common to all cruises within a
 year and were classified as being in the hypolimnion, initial DO
 concentrations and depletion rates were calculated and tests about their
 constancy were performed using weighted regression analysis and regression
 models with the time structure of the data explicitly incorporated in the
 models. The yearly uncorrected depletion rates for 1967-1980 were similar
 to values previously reported by several authors, indicating that this
 semi-objective **clustering** procedure provides a practical
 alternative to subjective selection of data. The conclusions about
 constancy of initial concentrations and depletion rates based on an
 unweighted regression analysis were shown to differ from those of weighted
 regression. Using regression with empirical weights, neither the initial
 DO concentration nor the depletion rate remained constant between 1967 and
 1980 in the Central Basin but the depletion rate remained constant and the
 initial DO concentration varied in the Eastern Basin.

L4 ANSWER 32 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1982:149074 BIOSIS
 DN PREV198273009058; BA73:9058
 TI **HIERARCHICAL** CLASSIFICATION OF COMMUNITY DATA.
 AU GAUCH H G JR [Reprint author]; WHITTAKER R H
 CS SECTION OF ECOLOGY SYSTEMATICS, CORNELL UNIV, ITHACA, NEW YORK 14850, USA
 SO Journal of Ecology, (1981) Vol. 69, No. 2, pp. 537-558.
 CODEN: JEEOAB. ISSN: 0022-0477.
 DT Article
 FS BA

LA ENGLISH
 AB The application of **hierarchical** classification to ecological community data is examined, using a variety of classification techniques and test data sets. Problems discussed include the choice of a conceptual space in which points representing samples or species or both are located; the effects of random noise and nonlinearity; the degree to which clusters are natural to a data set or are imposed by the **clustering** technique; the choice of criteria for locating divisions; **clustering** strategies (**non-hierarchical** vs. **hierarchical**, divisive vs. agglomerative and polythetic vs. monothetic); the presentation of results of various **clustering** techniques; and methods for evaluating and comparing **clustering** techniques and their results. Five **hierarchical clustering** techniques are compared: complete linkage **clustering**, the unweighted pair group method using arithmetic averages, minimization of within-group dispersion, 2-way indicator species analysis, and partitioning of an ordination space (using detrended correspondence analysis, a modification of reciprocal averaging). The first 3 techniques are agglomerative and the last 2 are divisive. Data sets for tests include simulated data sets in 1 to 4 dimensions (some incorporating noise of 3 kinds), and field data varying in number of samples, noise level and number and length of community gradients. Two-way indicator species analysis is usually the best, but there are cases in which other techniques may be complementary or superior. Theoretical requirements and test results are discussed to show why **clustering** of ecological community data is usually best approached by a divisive strategy. This conclusion is important because the analysis may be stopped after a limited number of divisions, thus needing less computation than do agglomerative strategies. The 2 divisive techniques discussed here have computer requirements which rise only linearly with the amount of data, making analysis of large data sets practical.

L4 ANSWER 33 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1982:243880 BIOSIS
 DN PREV198274016360; BA74:16360
 TI DISTRIBUTIONAL RELATIONS AND HOMOGENOUS AREAS IN AQUATIC MACROPHYTE VEGETATION A CASE STUDY.
 AU KURIMO H [Reprint author]; KURIMO U
 CS DEP GEOGRAPHY, UNIV JOENSUU, PO BOX 111, SF-80101 JOENSUU 10
 SO Annales Botanici Fennici, (1981) Vol. 18, No. 4, pp. 293-312.
 CODEN: ABOFAQ. ISSN: 0003-3847.
 DT Article
 FS BA
 LA ENGLISH
 AB The distributional relations of aquatic macrophytes were examined by correlation analysis and floristically homogeneous areas were delimited by multivariate principal component analysis and **non-hierarchical** agglomerative multivariate **clustering** (grouping) techniques, using data on the presence/absence and a buandance of the species. Species having the same or opposite distribution patterns and species that were evenly distributed throughout the waters were easily distinguished. Particular vegetationally homogeneous areas could be distinguished. The results remained largely the same when the data were treated differently or restricted. The data on the species' abundance make no important difference to the results yielded by the presence/absence data. The homogeneous areas delimited according to the

floristic similarities largely agreed with the areas distinguished on the basis of the environmental conditions, mainly water properties. The vegetation of the homogeneous areas was examined with respect to the occurrence of the life-forms and of categories of species indicate of the water quality. The results yield by the mathematical techniques agree well with those reached by convetional methods, **clustering** procedures are suitable for this kind of study, but complicated mathematical methods are not essential of reaching correct results. Average accuracy and reliability can be attained with only a selected fraction of the total vegetational data and general trends can be revealed using only a few indicator species.

L4 ANSWER 34 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1980:183429 BIOSIS
DN PREV198069058425; BA69:58425
TI DISTRIBUTION OF WESTERN BEAUFORT SEA ALASKA USA POLYCHAETOUS ANNELIDS.
AU BILYARD G R [Reprint author]; CAREY A G JR
CS SCH OCEANOGR, OREG STATE UNIV, CORVALLIS, OREG 97331, USA
SO Marine Biology (Berlin), (1979) Vol. 54, No. 4, pp. 329-340.
CODEN: MBIOAJ. ISSN: 0025-3162.
DT Article
FS BA
LA ENGLISH
AB Depth and depth-related processes appear to exert primary control over the distributional patterns of species of polychaetous annelids in the western Beaufort Sea (Cape Halkett-Barter Island, Alaska). Species richness and total polychaete abundance are maximal along the outer continental shelf and upper continental slope. Stations exhibiting the most similar polychaete assemblages are located at similar depths. Some species distributions appear to correlate better with sediment type than with depth. Maximum abundance occurs deeper on the continental slope to the west; and station clusters generated by **non-hierarchical clustering** (using the dominant polychaete species data) are not sorted strictly by depth. In a canonical analysis of discriminance, the station clusters were projected onto a 2 dimensional plane in species space. The 1st and 2nd canonical variables of the station clusters correlate with sediment grain-size distributions, suggesting a relationship between polychaete distribution patterns and the sedimentary environment. This relationship is further substantiated when sediment grain-size distributions for each station are plotted on a tertiary diagram: the stations are grouped and ordered in a pattern similar to that generated by the canonical analysis of discriminance.

L4 ANSWER 35 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1979:218683 BIOSIS
DN PREV197968021187; BA68:21187
TI VEGETATION OF THE ROYAL BOTANIC GARDENS ANNEX AT CRANBOURNE VICTORIA AUSTRALIA.
AU GULLAN P K [Reprint author]
CS NATL HERB, BIRDWOOD AVE, SOUTH YARRA, VICTORIA 3141, AUST
SO Proceedings of the Royal Society of Victoria, (1978) Vol. 90, No. 1-2, pp. 225-240.
CODEN: PRSVAV. ISSN: 0035-9211.
DT Article
FS BA
LA ENGLISH

AB The Royal Botanic Gardens Annexe at Cranbourne [Victoria, Australia] supports 200 ha of closed-heath, closed-scrub and low closed-forest (sensu Specht, 1970). Variation of the floristic composition of the vegetation is mostly continuous along topographic and edaphic gradients, but sharp discontinuities occur where permanent water is at, or close to, the soil surface. Studies made of regeneration after clearing suggests that if the topsoil is not removed floristic regeneration is complete within 8 yr, while structural regeneration may take up to 30 yr. A method for sorting 2-way tables for vegetation description is included. This method employs a polythetic, agglomerative, **non-hierarchical clustering** procedure, with a data editing facility.

=>

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	ENTRY	SESSION
FULL ESTIMATED COST	58.64	58.85

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NEWS	19	May 12	Polymer links for the POLYLINK command completed in REGISTRY
NEWS	20	May 17	FRFULL now available on STN
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FILE 'HOME' ENTERED AT 10:28:21 ON 24 MAY 2004

=> file .pub

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 10:28:30 ON 24 MAY 2004

FILE 'BIOSIS' ENTERED AT 10:28:30 ON 24 MAY 2004

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=> e skierczynski/au

E1	2	SKIERCZYNSKA A/AU
E2	9	SKIERCZYNSKA J/AU
E3	0 -->	SKIERCZYNSKI/AU
E4	1	SKIERCZYNSKI B/AU
E5	22	SKIERCZYNSKI B A/AU
E6	2	SKIERCZYNSKI BOGUSLAW A/AU
E7	2	SKIERCZYNSKI PAUL/AU
E8	2	SKIERCZYNSKI PAUL A/AU
E9	1	SKIERDE S/AU
E10	1	SKIERKA R L/AU
E11	2	SKIERKOWSKA B/AU
E12	2	SKIERKOWSKI J/AU

=> s e4-e6

L1 25 ("SKIERCZYNSKI B"/AU OR "SKIERCZYNSKI B A"/AU OR "SKIERCZYNSKI BOGUSLAW A"/AU)

=> s l1 and clustering

L2 0 L1 AND CLUSTERING

=> s l1 and hierarchical

L3 0 L1 AND HIERARCHICAL

=> e schork/au

E13	3	SCHORIN MARSHALL/AU
E14	4	SCHORIN MARSHALL A/AU
E15	0 -->	SCHORK/AU
E16	91	SCHORK A/AU
E17	5	SCHORK A M/AU
E18	2	SCHORK A R/AU
E19	13	SCHORK ANTHONY/AU
E20	2	SCHORK ANTHONY M/AU
E21	1	SCHORK ANTONY/AU
E22	2	SCHORK ASTRID/AU
E23	2	SCHORK C M/AU
E24	1	SCHORK CATHERINE M/AU

=> e schork n j/au

E25	53	SCHORK N/AU
E26	1	SCHORK N A/AU
E27	190 -->	SCHORK N J/AU
E28	1	SCHORK N M/AU
E29	6	SCHORK NICHOLAS/AU
E30	1	SCHORK NICHOLAS A/AU
E31	100	SCHORK NICHOLAS J/AU
E32	8	SCHORK P/AU
E33	5	SCHORK P K/AU
E34	1	SCHORK S/AU
E35	3	SCHORK S M/AU
E36	2	SCHORK STEFAN M/AU

=> s e27, ee29, e31

L4 190 E27, EE29, E31

=> s l4 and hierarchical

L5 0 L4 AND HIERARCHICAL

=>

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=> LOG Y

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FULL ESTIMATED COST	3.69	3.90

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NEWS 5 FEB 05 German (DE) application and patent publication number format
changes
NEWS 6 MAR 03 MEDLINE and LMEDLINE reloaded
NEWS 7 MAR 03 MEDLINE file segment of TOXCENTER reloaded
NEWS 8 MAR 03 FRANCEPAT now available on STN
NEWS 9 MAR 29 Pharmaceutical Substances (PS) now available on STN
NEWS 10 MAR 29 WPIFV now available on STN
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NEWS 15 APR 27 NLDB: New search and display fields available
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and June 2004
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MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004
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COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 10:33:43 ON 24 MAY 2004

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=> s hierarchical and non-hierarchical

L1 150 HIERARCHICAL AND NON-HIERARCHICAL

=> s l1 and cluster

L2 50 L1 AND CLUSTER

=> s hierarchical and "non-hierarchical"

L3 150 HIERARCHICAL AND "NON-HIERARCHICAL"

=> s l3 and cluster

L4 50 L3 AND CLUSTER

=> duplicate remove l4

DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'

KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L4

L5 48 DUPLICATE REMOVE L4 (2 DUPLICATES REMOVED)

=> s l5 and py<2000

L6 33 L5 AND PY<2000

=> d 1-33 bib ab

L6 ANSWER 1 OF 33 MEDLINE on STN

AN 1998178077 MEDLINE

DN PubMed ID: 9517009

TI An evaluation of structural descriptors and clustering methods for use in diversity selection.

AU Brown R D; Martin Y C

CS Pharmaceutical Products Division, Abbott Laboratories, Abbott Park, IL 60064-350, USA.

SO SAR and QSAR in environmental research, (1998) 8 (1-2) 23-39.
Journal code: 9440156. ISSN: 1062-936X.

CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199804

ED Entered STN: 19980507
 Last Updated on STN: 19980507
 Entered Medline: 19980429

AB An evaluation of the suitability of a number of structural descriptors and clustering methods for use in diversity selection is presented. The methods are compared by their success in simulated biological activity predictions. The results suggest that simple 2D structural descriptors are particularly effective and that **hierarchical** clustering methods are superior to the **non-hierarchical** methods traditionally used for diversity related tasks. Results are presented which suggest that the difference in the utility of the descriptors can be accounted for by the different extent to which each encodes information relevant to the forces of ligand-receptor binding.

L6 ANSWER 2 OF 33 MEDLINE on STN
 AN 94084457 MEDLINE
 DN PubMed ID: 1341650
 TI **Cluster** analysis and related techniques in medical research.
 AU McLachlan G J
 CS Department of Mathematics, University of Queensland, Australia.
 SO Statistical methods in medical research, (1992) 1 (1) 27-48.
 Ref: 54
 Journal code: 9212457. ISSN: 0962-2802.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, ACADEMIC)
 LA English
 FS Priority Journals
 EM 199401
 ED Entered STN: 19940209
 Last Updated on STN: 19990129
 Entered Medline: 19940127

AB In this paper we review methods of **cluster** analysis in the context of classifying patients on the basis of clinical and/or laboratory type observations. Both **hierarchical** and **non-hierarchical** methods of clustering are considered, although the emphasis is on the latter type, with particular attention devoted to the mixture likelihood-based approach. For the purposes of dividing a given data set into **g clusters**, this approach fits a mixture model of **g** components, using the method of maximum likelihood. It thus provides a sound statistical basis for clustering. The important but difficult question of how many **clusters** are there in the data can be addressed within the framework of standard statistical theory, although theoretical and computational difficulties still remain. Two case studies, involving the **cluster** analysis of some haemophilia and diabetes data respectively, are reported to demonstrate the mixture likelihood-based approach to clustering.

L6 ANSWER 3 OF 33 MEDLINE on STN
 AN 89249858 MEDLINE
 DN PubMed ID: 2720980
 TI Statistical interpretation of concentrations of magnesium, zinc, calcium, potassium, cholesterols, and creatine kinase isoenzymes in men at different stages of ischemic heart disease.
 AU Speich M; Auget J L; Arnaud P

CS Laboratoire de Biochimie Pharmaceutique, Faculte de Pharmacie, Nantes,
France.

SO Clinical chemistry, (1989 May) 35 (5) 833-5.
Journal code: 9421549. ISSN: 0009-9147.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 198907

ED Entered STN: 19900306
Last Updated on STN: 19970203
Entered Medline: 19890706

AB We present a statistical interpretation of plasma (Pl) and (or)
erythrocyte (Erc) concentrations of magnesium, zinc, calcium, potassium,
and total high-density lipoprotein (HDL) cholesterol, as well as of the
activity of total creatine kinase (CK) and its CK-MB isoenzyme, in 26 men
with pre-infarction syndrome (PIS) and 34 men with acute myocardial
infarction (MI). Discriminant analysis allowed overall comparison of both
groups and determination of the most significant variables: CK and Pl-Zn.
By **non-hierarchical cluster** analysis we
defined three homogeneous subgroups among MI men, with CK, CK-MB, and
Pl-Zn differing significantly between the groups. In PIS men, Pl-Zn was
correlated with Pl-Ca, whereas in MI men Pl-Zn was correlated with Pl-Mg.
Stepwise regression indicated that Pl-Zn was the most significant
regressor of CK in PIS men and of CK-MB in MI men. All these statistical
interpretations support a special role of Pl-Zn in diagnosis and perhaps
prognosis. After MI, interleukin-1 release may possibly mediate observed
hypo-zincemia via formation of a heart Zn-metallothionein.

L6 ANSWER 4 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 2001:425911 BIOSIS

DN PREV200100425911

TI Genetic diversity in relation to number of **clusters** in wheat
(Triticum aestivum).

AU Suri, Vishal [Reprint author]; Sharma, S. C. [Reprint author]

CS Department of Genetics, Punjab Agricultural University, Ludhiana, 141 004,
USA

SO Crop Improvement, (December, 1999) Vol. 26, No. 2, pp. 208-215. print.
ISSN: 0256-0933.

DT Article

LA English

ED Entered STN: 12 Sep 2001
Last Updated on STN: 22 Feb 2002

AB In the present investigation 200 genotypes of wheat (Triticum aestivum)
have been grouped into sixteen **clusters** using Mahalanobis D2
statsitics, based on eight morphological characters namely; days to
flowering, tiller number, plant height, 1000-grain weight, grains/ear,
biological yield and harvest index. The genetic divergence was
independent of pedigree as well as place of origin/place of release.
Grain yield and tiller number were major contributors towards genetics
divergence with moderate contribution from 1000-grain weight, grains/ear
and harvest index. Grain yield was significantly and positively
correlated with the component traits except plant height and days to
flowering. Non-hierarchical Euclidean **cluster** analysis was also
used to group 200 genotype into different number of **clusters**
ranging from 2-16. Out of varying number of **clusters** (2 to 16),

the one with 10-**clusters** was taken as no major differences either in mean cv values or their range were observed which suggested that grouping 200 genotypes into 10-**clusters** was as effective as that of 16-**clusters** without any loss of information.

L6 ANSWER 5 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:480550 BIOSIS
DN PREV199900480550
TI Eco-geographical diversity vis-a-vis agromorphological divergence in germplasm of forage maize (*Zea mays* L.).
AU Katiyar, P. K. [Reprint author]; Choubey, R. N. [Reprint author]; Chaudhary, B. S. [Reprint author]
CS Indian Grassland and Fodder Research Institute, Jhansi, 284 003, India
SO Crop Improvement, (Dec., 1998) Vol. 25, No. 2, pp. 191-196. print. ISSN: 0256-0933.
DT Article
LA English
ED Entered STN: 16 Nov 1999
Last Updated on STN: 16 Nov 1999
AB Three hundred genotypes of fodder types in maize (*Zea mays* L.) of diverse eco-geographical origin were evaluated for genetic variability. Principal component and **non-hierarchical** Euclidean **cluster** analysis was used to compare the genotypes. Accessions were classified into 12 broad groups. Group E was the largest consisting of 35 accessions, while minimum number (18 accessions) was observed in **cluster** J. There was no parallelism between genetic and geographical diversity. The hybridization programme based on such analysis has been suggested which is likely to prove fruitful in fodder maize improvement programme.

L6 ANSWER 6 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:253766 BIOSIS
DN PREV199900253766
TI Use of **cluster** analysis to validate IHS diagnostic criteria for migraine and tension-type headache.
AU Bruehl, Stephen [Reprint author]; Lofland, Kenneth R.; Semenchuk, Elizabeth M.; Rokicki, Lori A.; Penzien, Donald B.
CS Center for Pain Studies, Rehabilitation Institute of Chicago, 345 East Superior Street, Room 904, Chicago, IL, 60611, USA
SO Headache, (March, 1999) Vol. 39, No. 3, pp. 181-189. print. CODEN: HEADAE. ISSN: 0017-8748.
DT Article
LA English
ED Entered STN: 2 Jul 1999
Last Updated on STN: 2 Jul 1999
AB **Cluster** analysis was used to validate headache diagnostic criteria of the International Headache Society (IHS). Structured diagnostic interviews were conducted on 443 headache sufferers from a community sample, which was randomly split to allow replication. **Hierarchical cluster** analysis of symptoms in both subsamples revealed two distinct ($P < .001$) **clusters**: (1) unilateral pulsating pain, pain aggravated by activity, and photophobia and phonophobia, and (2) bilateral pressing/tightening pain, mild to moderate intensity, and absence of nausea/vomiting. These **clusters** were consistent with IHS migraine and tension-type classifications, respectively. Replication using a **non-**

hierarchical clustering technique, k-means **cluster** analysis, revealed a migrainelike patient **cluster**, reflecting more frequent pulsating, unilateral pain; more severe pain; and pain aggravated by activity; nausea, vomiting, photophobia, and phonophobia. A tensionlike patient **cluster** was also identified, reflecting more frequent pressing/tightening pain, mild to moderate pain, bilateral location, and absence of nausea/vomiting. These patient **clusters** were consistent across subsamples. International Headache Society diagnoses corresponded with classification based upon statistically derived **clusters** ($P < .001$). These results indicate that headache symptoms **cluster** empirically in a manner consistent with IHS criteria for migraine and tension-type headaches. Criterion overlap problems regarding pain intensity and duration were identified. Overall, these data support migraine and tension-type headache as distinct entities, and provide support for the IHS diagnostic criteria with minor modifications.

L6 ANSWER 7 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:238053 BIOSIS
DN PREV199900238053
TI Classification and receptor modeling of wet precipitation data from Central Austria (1984-1993).
AU Simeonov, V. [Reprint author]; Puxbaum, H.; Tsakovski, S.; Sarbu, C.; Kalina, M.
CS Faculty of Chemistry, University of Sofia 'St. Kliment Okhridski', J. Bourchier Blvd. 1, 1126, Sofia, Bulgaria
SO Environmetrics, (March-April, 1999) Vol. 10, No. 2, pp. 137-152. print. ISSN: 1180-4009.
DT Article
LA English
ED Entered STN: 17 Jun 1999
Last Updated on STN: 17 Jun 1999
AB Various classification procedures (**hierarchical** and **non-hierarchical** crisp and fuzzy clustering, cross-classification fuzzy clustering) and principal component analysis (varimax rotation) combined with receptor modeling are applied to a data set consisting of wet deposition loads of major ions from five sampling sites in Central Austria collected in a period of 10 years (1984-1993). The data classification with respect to the sampling sites as objects has shown that a distinct separation between sites located at the northern Alpine rim (Reutte, Kufstein and Haunsberg) and in the inner Alpine region (Innervillgraten and Werfenweng) is achieved indicating in this way the role of the geographical disposition of the sampling sites. Both **cluster** and principal components analysis proved that three conditional (latent) factors are responsible for the data structure called in this study 'anthropogenic', 'crustal' and 'mixed salt' - (NH_4^+ , SO_4^{2-} , NO_3^- , H^+), (Ca^{2+} , Mg^{2+}), (K^+ , Na^+ , Cl^-), respectively. The source apportioning model has indicated that anthropogenic gaseous emissions might be responsible for the first factor, natural crustal influences and Sahara events for the second and sea salt and manure for the third.

L6 ANSWER 8 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:47046 BIOSIS
DN PREV199900047046
TI Genetic diversity in a large collection of wheats (*Triticum* spp.).
AU Sharma, P. K.; Gupta, P. K.; Balyan, H. S.

CS Dep. Agric. Botany, C. Charan Singh Univ., Meerut 250 004, India
 SO Indian Journal of Genetics and Plant Breeding, (Aug., 1998) Vol. 58, No. 3, pp. 271-278. print.
 CODEN: IJGBAG. ISSN: 0019-5200.

DT Article
 LA English
 ED Entered STN: 10 Feb 1999
 Last Updated on STN: 10 Feb 1999

AB Three hundred genotypes of bread and durum wheats including Indian and exotic collections were evaluated for 10 yield and other related characters. Five characters (grain and biological yields, tiller number, grain weight/ear and grains/ear) exhibited high variability. Of the remaining five traits, flag leaf area and 100-grain weight showed moderate variability while plant height, peduncle length and harvest index showed relatively low variability. Following the **non-hierarchical** euclidean **cluster** analysis, all the 300 genotypes were grouped into 16 **clusters** with variable number of genotypes. Genotypes of heterogeneous origin/place of release, and of different ploidy levels (bread and durum wheats) often grouped together in the same **cluster**, suggesting some degree of ancestral relationship between the genotypes. This also suggested a lack of relationship between the genetic diversity and the ploidy level of genotypes. On the basis of the data on genetic divergence and mean performance of yield and other traits, five diverse and superior genotypes, namely MUW 109, CPAN 3064, CPAN 1556, MUW 104, and CPAN 1998 were selected. Each of these genotypes was exceptionally good for one or more characters and was reasonable for other characters relatives to those of the best check varieties. Therefore, these genotypes may be involved in multiple crossing programme to recover transgressive segregates. Further, on the basis of character associations, it is argued that selection of plants with high biological yield coupled with optimum harvest index (50%) should result in progenies with high grain yield potential in wheat.

L6 ANSWER 9 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1998:134894 BIOSIS
 DN PREV199800134894
 TI Artificial neural network technology for the classification and cartography of scientific and technical information.

AU Polanco, X.; Francois, Claire; Keim, J.-P.
 CS Programme Rech. Infometrie, Inst. Inform. Sci. Technique, Cent. Natl. Rech. Sci., 2 allée Parc de Brabois, 54514 Vandoeuvre Nancy Cedex, France
 SO Scientometrics, (Jan.-Feb., 1998) Vol. 41, No. 1-2, pp. 69-82. print.
 CODEN: SCNTDX. ISSN: 0138-9130.

DT Article
 LA English
 ED Entered STN: 20 Mar 1998
 Last Updated on STN: 20 Mar 1998

AB This paper describes the implementation of multivariate data analysis: NEURODOC applies the axial k-means method for automatic, **non-hierarchical cluster** analysis and a Principal Component Analysis (PCA) for representing the **clusters** on a map. We next introduce Artificial Neural Networks (ANNs) to extend NEURODOC into a neural platform for the **cluster** analysis and cartography of bibliographic data. The ANNs tested are: the Adaptive Resonance Theory (ART 1), a Multilayer Perceptron (MLP), and an associative network with

unsupervised learning (KOHONEN). This platform is intended for quantitative analysis of information.

L6 ANSWER 10 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:339158 BIOSIS
DN PREV199799638361
TI The analysis of large scale data taken from the world groundnut (*Arachis hypogaea* L.) germplasm collection: I. Two-way quantitative data.
AU Harch, B. D. [Reprint author]; Basford, K. E.; Delacy, I. H.; Lawrence, P. K.
CS CSIRO, Math. Inf. Sci., PMB 2, Glen Osmond, SA 5064, Australia
SO Euphytica, (1997) Vol. 95, No. 1, pp. 27-38.
CODEN: EUPHAA. ISSN: 0014-2336.
DT Article
LA English
ED Entered STN: 11 Aug 1997
Last Updated on STN: 11 Aug 1997
AB Data associated with germplasm collections are typically large and multivariate with a considerable number of descriptors measured on each of many accessions. Pattern analysis methods of clustering and ordination have been identified as techniques for statistically evaluating the available diversity in germplasm data. While used in many studies, the approaches have not dealt explicitly with the computational consequences of large data sets (i.e. greater than 5000 accessions). To consider the application of these techniques to germplasm evaluation data, 11328 accessions of groundnut (*Arachis hypogaea* L) from the International Research Institute for the Semi-Arid Tropics, Andhra Pradesh, India were examined. Data for nine quantitative descriptors measured in the rainy and post-rainy growing seasons were used. The ordination technique of principal component analysis was used to reduce the dimensionality of the germplasm data. The identification of phenotypically similar groups of accessions within large scale data via the computationally intensive **hierarchical** clustering techniques was not feasible and **non-hierarchical** techniques had to be used. Finite mixture models that maximise the likelihood of an accession belonging to a **cluster** were used to **cluster** the accessions in this collection. The patterns of response for the different growing seasons were found to be highly correlated. However, in relating the results to passport and other characterisation and evaluation descriptors, the observed patterns did not appear to be related to taxonomy or any other well known characteristics of groundnut.

L6 ANSWER 11 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:217318 BIOSIS
DN PREV199799523822
TI Components of relative growth rate and their interrelations in 59 temperate plant species.
AU Hunt, Roderick [Reprint author]; Cornelissen, J. H. C.
CS NERC Unit Comparative Plant Ecol., Dep. Animal Plant Sci., Univ. Sheffield, Sheffield S10 2TN, UK
SO New Phytologist, (1997) Vol. 135, No. 3, pp. 395-417.
CODEN: NEPHAV. ISSN: 0028-646X.
DT Article
LA English
ED Entered STN: 22 May 1997
Last Updated on STN: 22 May 1997

AB Three groups of species (21 herbaceous monocotyledons, 22 herbaceous dicotyledons and 16 woody dicotyledons), including representatives of a wide range of natural habitats and life forms in inland Britain, were grown in the seedling phase in a resource-rich controlled environment and assessed over a 14-day period (21 d in the case of woody species). Mean values of relative growth rate (RGR), unit leaf rate (ULR), leaf area ratio (LAR), leaf weight fraction (LWF), specific leaf area (SLA), and the root-shoot allometric coefficient were derived. In herbaceous species, the grand mean RGR was 0.20 d⁻¹, comparable to values previously recorded. For woody species, the mean was 0.09 d⁻¹. An existing assumption linking high RGR to high allocation to photosynthetic biomass was upheld by comparisons made between groups. Within groups, however, no pattern of this kind could be demonstrated. When photosynthetically active radiation was increased from 125 to 250 $\mu\text{mol m}^{-2} \text{s}^{-1}$, ULR was increased almost pro rata. The parallel response in RGR was only slight, being offset by considerable reductions in LAR. The apparent mean quantum yield for photosynthesis in herbaceous species (whole-plant d. wt basis) was 0.60 g mol⁻¹. There was no significant dependence of RGR on ULR in any of the three groups of species, although the absolute magnitude of ULR declined in the order: herbaceous monocotyledons > herbaceous dicotyledons > woody dicotyledons. In all three groups, RGR was strongly dependent upon LAR but no differences emerged in absolute scale of LAR. The absolute scale of mean LWF decreased from herbaceous to woody species, but the dependence of LAR on LWF strengthened. Groups showed no systematic differences in magnitude of SLA, but the correlation of LAR with SLA was strong throughout. Multiple regression showed that the leading determinants of RGR were ULR and SLA in herbaceous species and LWF in woody species. Principal components analyses (PCA) on each of the three groups explained at least 77% of variation and agreed closely with an optimal (**non-hierarchical**) classification. Only six **cluster** 'types' were recognized out of the 16 theoretically possible combinations of 'high' or 'low' values of the four growth parameters. Strong evidence of evolutionary trade-offs emerged, most strikingly in that high RGR was never seen in combination with low SLA. The morphological/physiological types identified by an all-groups PCA separated woody from the herbaceous species, but dicotyledons were almost congruent with the monocotyledons. The non-growth-analytical attributes most strongly correlated with mean RGR were percentage yield at a low level of mineral nutrients, leaf nitrogen concentration, and seed weight. It was concluded that mean RGR plays a central role in the identification of pathways of evolutionary specialization in herbaceous species.

L6 ANSWER 12 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:198429 BIOSIS
DN PREV199799497632
TI Evaluation of genetic divergence in wheat (*Triticum aestivum* L.)
germplasm.
AU Walia, D. P. [Reprint author]; Garg, D. K.
CS Dep. Fruit Breeding, Univ. Horticulture Forestry, Nauni, Solan 173 230,
India
SO Indian Journal of Genetics and Plant Breeding, (1996) Vol. 56, No. 4, pp.
452-457.
CODEN: IJGBAG. ISSN: 0019-5200.
DT Article
LA English
ED Entered STN: 12 May 1997

Last Updated on STN: 12 May 1997

AB The nature and magnitude of genetic diversity was assessed using **non-hierarchical** euclidean **cluster** analysis in 405 pure breeding lines of *T. aestivum* for grain yield and its associated traits. All the genotypes got grouped in 13 different **clusters**. The clustering pattern of the genotypes belonging to the same country revealed their distribution in more than one **cluster** showing nonparallelism between geographic and genetic diversity. Members of **cluster** IV and IX were highly diverse from each other. **Cluster** VI had high mean values for grain yield, biological yield, number of tillers/unit area and harvest index. A number of genotypes were also identified which may serve as potent genetic donors for some metric traits.

L6 ANSWER 13 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1996:573845 BIOSIS

DN PREV199799288526

TI Floristic patterns and phytogeography of Skane, S Sweden.

AU Andersson, Per-Arne [Reprint author]; Weimarck, Gunnar

CS Dep. Ecological Botany, Villavagen 14, S-752 36 Uppsala, Sweden

SO Acta Universitatis Upsaliensis Symbolae Botanicae Upsalienses, (1996) Vol. 31, No. 3, pp. 239-264.

CODEN: SBUPAC. ISSN: 0082-0644.

DT Article

LA English

ED Entered STN: 23 Dec 1996

Last Updated on STN: 23 Dec 1996

AB Dot maps of the distribution of 895 vascular plant taxa in the province of Skane, S Sweden, were digitized and the records assigned to 483 quadrats of 5 times 5 km each. Quadrats and species were classified by the **non-hierarchical** agglomerative clustering program TABORD and ordinated by the program DECORANA. The results are given in a phytosociological table and as grid map plots and ordination graphs. Gradients are interpreted and **clusters** described in terms of Ellenberg's indicator scores. A regional floristic subdivision of the province in eight areas is proposed. The position of the border, 'limes scanicus', between two previously proposed major areas is modified here.

L6 ANSWER 14 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1996:283806 BIOSIS

DN PREV199699006162

TI Genetic divergence in greengram (*Phaseolus radiatus*) germplasm through use of **non-hierarchical** Euclidean **cluster** analysis.

AU Sharma, B. L. [Reprint author]; Singh, D. P.; Ram, H. H.

CS Dep. Genetics Plant Breeding, Pantnagar, Uttar Pradesh 263 145, India

SO Indian Journal of Agricultural Sciences, (1996) Vol. 66, No. 3, pp. 193-196.

CODEN: IJASA3. ISSN: 0019-5022.

DT Article

LA English

ED Entered STN: 25 Jun 1996

Last Updated on STN: 25 Jun 1996

L6 ANSWER 15 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1996:238517 BIOSIS

DN PREV199698786646

TI Comparative anatomy of the wood of *Quercus affinis* and *Q. laurina* (Fagaceae).

AU Valencia Avalos, Susana [Reprint author]; Barajas-Morales, Josefina

CS Herbario FCME, Fac. Ciencias, UNAM, Apdo. Postal 70-399, Del. Coyacan, 04510 Mexico, D.F., Mexico

SO Anales del Instituto de Biologia Universidad Nacional Autonoma de Mexico Serie Botanica, (1995) Vol. 66, No. 2, pp. 113-131. CODEN: AMXSAH. ISSN: 0374-5511.

DT Article

LA Spanish

ED Entered STN: 28 May 1996
Last Updated on STN: 28 May 1996

AB *Quercus affinis* Scheidweiler and *Quercus laurina* Humboldt et Bonpland, are morphologically very similar making their identification very difficult. Their wood anatomy was studied in order to use it as an aid in a more precise identification. The anatomical qualitative and quantitative characteristics of the wood of both species were compared, using the data of *Q. acherdophylla* as a standard reference. The macroscopic and microscopic data were compared using **non hierarchical** statistics tests of discriminant analysis and by the technique of **cluster** average league (UPGMA). The results confirm the existence of two well differentiated taxa, *Q. affinis* and *Q. laurina*, and an intermediate group that we are calling *Q. affinis* times *Q. laurina* from the neovolcanic axis. The anatomical traits more useful in delimiting taxa are porosity type, growth rings, sapwood color, grain type, fiber length, vessel diameter, and width of multiseriate rays.

L6 ANSWER 16 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1996:21659 BIOSIS

DN PREV199698593794

TI Genetic diversity in South Asian okra (*Abelmoschus esculentus*) germplasm collection.

AU Bisht, I. S.; Mahajan, R. K.; Rana, R. S.

CS Natl. Bureau Plant Genetic Resources, Pusa Campus, New Delhi 110012, India

SO Annals of Applied Biology, (1995) Vol. 126, No. 3, pp. 539-550. CODEN: AABIAV. ISSN: 0003-4746.

DT Article

LA English

ED Entered STN: 12 Jan 1996
Last Updated on STN: 12 Jan 1996

AB Genetic diversity for a range of morphological characters within 260 accessions of okra collected from India, Bangladesh, Nepal and Sri Lanka was investigated through the use of uni-, bi- and multivariate statistics. The pubescence and pigmentation of various plant parts, among qualitative descriptors, seemed to be most significant in the analysis of variability. The multivariate analysis, mainly on quantitative descriptors, using principal component and **non-hierarchical cluster** analysis suggested that days to flowering, plant height, and various fruit characteristics were important components of variability and contributed significantly to the total variation observed. Only two of the 10 principal components had eigen values more than 1 and together accounted for 54.52% of the total variation. The accessions were grouped into eight distinct **clusters** which further emphasized the relative contribution of various quantitative characters to the total variability. The pattern of genetic variation is of great importance both

to germplasm collectors and plant breeders. Specific accessions were also identified that could be passed on to breeders for utilization in crop improvement programme.

L6 ANSWER 17 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1994:526576 BIOSIS
DN PREV199497539576
TI Computer-assisted mapping of paddy-field soils: II. Classification,
mapping and significance.
AU Ishida, Tomoyuki [Reprint author]; Ando, Ho
CS Fac. Agric., Kagawa Univ., Kida-gun, Kagawa 761-07, Japan
SO Soil Science and Plant Nutrition, (1994) Vol. 40, No. 3, pp. 403-414.
CODEN: SSPNAW. ISSN: 0038-0768.
DT Article
LA English
ED Entered STN: 15 Dec 1994
Last Updated on STN: 16 Dec 1994
AB In order to determine how a conventional soil map on a local scale can be reproduced from soil sample information, a set of numerical procedures was applied to the soil chemical data from 159 soil samples collected in paddy fields of the Aizu Basin, in the northern part of Japan. The digital elevation data were also included as an attribute. Various steps were involved. In the first step, the sparse data were converted into a closely spaced data set. This first step was previously described in Part I of this paper. In the second step a multivariate ordination (principal component analysis) was applied to the sampling data in order to avoid redundancy of information. Large contributions to the first component were derived from the values of CEC and exchangeable Ca and Mg. In the third step the sampling sites were numerically classified using the results of four or five components obtained in the second step. A **hierarchical** clustering method was applied to provide the initial set of **clusters** for **non-hierarchical** clustering. In the fourth step the closely spaced data collected in the first step were allocated to an appropriate class obtained by using the **non-hierarchical** clustering method applied in the third step. For the allocation method, the geographic location of the sampling sites was included as an additional characteristic of the data. In the regional partition map based on the numerical procedures, each soil group corresponded to a soil series in the original conventional soil map which depended predominantly on detailed morphological and topographical differences. In addition, the regional partition map was found to provide useful information for the identification of factors closely related to soil fertility, by statistically examining the differences in rice yield among the soil groups.

L6 ANSWER 18 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1994:346196 BIOSIS
DN PREV199497359196
TI The effects of osmotic pre-sowing treatment on laboratory germination in a range of wild flower species.
AU Tallwin, J. R. B.; Rook, A. J.; Brookman, S. K. E.
CS AFRC Inst. Grassland and Environmental Res., North Wyke Res. Station, Okehampton, Devon, EX20 2SB, UK
SO Annals of Applied Biology, (1994) Vol. 124, No. 2, pp. 363-370.
CODEN: AABIAV. ISSN: 0003-4746.
DT Article

LA English
ED Entered STN: 8 Aug 1994
Last Updated on STN: 8 Aug 1994
AB Sown seed of many wild flower species have slow or delayed germination which can allow unsown and undesirable species to colonize a prepared site. Ideally all seed sown should germinate immediately. Priming seed in an inert osmoticum can improve synchronization and speed of germination. The objective of this study was to assess the efficacy of priming on a selection of 60 wild flower species from a total of 21 different families. The majority of the species selected were common constituents of commercial seed mixtures. Seeds were primed in the light at 15 degree C for 14 days in a polyethylene glycol '6000' solution giving an osmotic potential of either -10 or -15 bars. Priming had a highly significant effect on speed of germination reducing the median germination time by 2.8 +/- 0.27 days in the -10 bar treatment and 1.6 +/- 0.27 days in the -15 bar treatment. At the species level, 28 species had significantly reduced median germination times following priming. Priming significantly enhanced the final germination percentage in 15 species and significantly reduced it in eight species, with the adverse effect being more pronounced at -15 bars than at -10 bars. **Non-hierarchical cluster** analysis showed no clear patterns in response to priming either in relation to the comparative ecology or the plant family of the species tested, with the possible exception of the Leguminosae species. Only one out of six members of this family showed any enhancement in germination rate or percentage. The study demonstrates that a priming treatment could improve speed of germination. in a wide range of commonly sown semi-natural grassland species.

L6 ANSWER 19 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1994:345339 BIOSIS
DN PREV199497358339
TI Application of multivariate analysis to site quality evaluation for coniferous plantations.
AU Ares, Adrian
CS Dep. Agronomy Soil Sci., Univ. Hawaii at Manoa, 1910 East-West Road, Honolulu, HI 96822, USA
SO South African Forestry Journal, (1993) Vol. 0, No. 167, pp. 27-34. CODEN: SAFJBF. ISSN: 0038-2167.
DT Article
LA English
ED Entered STN: 8 Aug 1994
Last Updated on STN: 8 Aug 1994
AB Multivariate analysis was performed on tree growth and environmental data from sites afforested with conifers in Ventania, southern Buenos Aires, Argentina. Pinus halepensis was investigated in 22 sites, Pinus radiata in 20 sites and Cedrus deodara and Cupressus sempervirens f. horizontalis in 15 sites each. Site index expressed as height of dominants at age 25 years was used as growth indicator. Four site quality classes were set up for each of the four species. Twenty three topographic and soil characteristics were used to group the sites into six groups by means of a **non-hierarchical cluster** analysis technique. The groups were then used to test the ability of the environmental variables to discriminate among site quality classes. Standardised mean site index of stands on cumulic soils were significantly higher than those on shallow soils. A **hierarchical** technique used to establish intergroup relationships produced similar results to **cluster**

analysis. Seven variables were selected as potential discriminators between growth response groups for all the species studied. Only rooting depth and depth to C horizon, rock or calcium carbonate layer, were finally selected as discriminators. It is concluded that rooting depth should be used as primary discriminant among sites in land evaluation for forestry in the region.

- L6 ANSWER 20 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1993:386396 BIOSIS
DN PREV199396061696
TI Comparing three classification strategies for use in ecology.
AU Belbin, Lee [Reprint author]; McDonald, Cam
CS CSIRO Div. Wildlife and Ecol., PO Box 84, Lyneham, ACT Australia 2602, australia
SO Journal of Vegetation Science, (1993) Vol. 4, No. 3, pp. 341-348.
CODEN: JVESEK. ISSN: 1100-9233.
DT Article
LA English
ED Entered STN: 23 Aug 1993
Last Updated on STN: 23 Aug 1993
AB We compare three common types of clustering algorithms for use with community data. TWINSpan is divisive **hierarchical**, flexible-UPGMA is agglomerative and **hierarchical**, and ALOC is **non-hierarchical**. A balanced design six-factor model was used to generate 480 data sets of known characteristics. Recovery of the embedded **clusters** suggests that both flexible UPGMA and ALOC are significantly better than TWINSpan. No significant difference existed between flexible UPGMA and ALOC.
- L6 ANSWER 21 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1992:285821 BIOSIS
DN PREV199294010471; BA94:10471
TI ELECTRON MICROPROBE CHARACTERIZATION OF INDIVIDUAL AEROSOL PARTICLES COLLECTED BY AIRCRAFT ABOVE THE SOUTHERN BIGHT OF THE NORTH SEA.
AU ROJAS C M [Reprint author]; VAN GRIEKEN R E
CS DEP CHEM, UNIV ANTWERP, UNIVERSITEITSPLEIN 1, B-2610 ANTWERP-WILRIJK, BELGIUM
SO Atmospheric Environment Part A General Topics, (1992) Vol. 26, No. 7, pp. 1231-1237.
CODEN: AEATEN. ISSN: 0960-1686.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 10 Jun 1992
Last Updated on STN: 10 Jun 1992
AB About 50,000 individual aerosol particles from a total of 108 samples collected at six different altitudes above the Southern Bight of the North Sea, have been analyzed using electron probe X-ray microanalysis. The results of **hierarchical cluster** analysis on each sample revealed that, for continental air masses, most of the aerosol particulate matter is characterized by high amounts of aluminosilicates, CaSO₄ and Fe-rich particles. For western and marine air masses there was no change in the composition of the most abundant particle type with height. This is in connection with the rather mixed nature of the atmosphere. **Non-hierarchical cluster** analysis showed that the most abundant particle types in this airshed are:

aluminosilicates from coal combustion releases, Fe-rich, sea salts enriched with Pb, and organic material associated with residual oil combustion tracers, accounting for 21, 16, 15 and 12% of the total analyzed particles, respectively. Almost 60% of the analyzed particles is related to combustion or energy-generation processes. Principal factor analysis on an elemental frequency matrix led to comparable results with principal factor analysis used in combination with **cluster** analysis. This shows that the method described here is useful for the identification of aerosol sources.

L6 ANSWER 22 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1992:53871 BIOSIS
DN PREV199293033846; BA93:33846
TI AN EMPIRICAL EVALUATION OF THE MBTI TYPOLOGY.
AU LORR M [Reprint author]
CS LIFE CYCLE INSTITUTE, THE CATHOLIC UNIV OF AMERICA, WASHINGTON, DC 20064,
USA
SO Personality and Individual Differences, (1991) Vol. 12, No. 11, pp.
1141-1146.
ISSN: 0191-8869.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 13 Jan 1992
Last Updated on STN: 13 Jan 1992
AB The popular Myers-Briggs Type Indicator (MBTI) applies a classification
schema that allocates all respondents to one of 16 types on the basis of
four preference scores. The study's aim was to evaluate the empirical
validity of the MBTI classification scheme. The approach taken was to
apply two **cluster** analytic procedures to the four standardized
scale scores. One method applied was Ward's **hierarchical**
grouping procedure and the other a **non-hierarchical**
average linkage. Five **clusters** in the first sample of 100 men
could be matched across the two procedures, and four **clusters** in
the second sample of 100 were also matched. On the whole, agreement
between the MBTI 16 categories and the empirically derived
clusters was weak or negligible. Some reasons why the MBTI
typology is defective as a classification scheme are carefully delineated.

L6 ANSWER 23 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1990:376848 BIOSIS
DN PREV199090063529; BA90:63529
TI ALLOMETRY IN LITHODES-ANTARCTICUS JACQUINOT 1983 CRUSTACEA DECAPODA LENGTH
OF THE RIGHT CHELA VERSUS CARAPACE LENGTH.
AU GUZMAN-M L [Reprint author]; RIOS-C C
CS AREA DE BIOL, INST DE LA PATAGONIA, UNIV DE MAGALLANES, CASILLA 113-D,
PUNTA ARENAS, CHILE
SO Anales del Instituto de la Patagonia Serie Ciencias Naturales, (1987) Vol.
17, pp. 89-98.
ISSN: 0716-6486.
DT Article
FS BA
LA SPANISH
ED Entered STN: 21 Aug 1990
Last Updated on STN: 21 Aug 1990
AB Right chela length and carapace length relationship in males of Lithodes

antarcticus Jacquinet 1853, from five fishing areas of the Magellan region (between 50° and 54° 30' S.L.) was studied. Specimens were collected approximately up to 60 m depth, between September-October 1980 and January-February 1984. Information was analyzed using a regression analysis applying the linearized allometric growth equation. Data from juveniles (immatures) and adults (matures) were studied separately. Due to individual variability, there is a size range, where immature and mature specimens overlap. Specimens from this range were classified according to a morphometric criterion, using a technique similar to a **non hierarchical cluster** analysis. Relative growth between both body structures is isometric in the juvenile phase, and allometric during the adult phase. This growth pattern is associated to sexual maturity, being the chela length increase about 15% higher during the adult phase. Juveniles from the five study areas showed a homogenous relative growth rate, and a similar results was obtained for adults. Thus, a common regression for each growth phase was calculated. Differences between studied stocks are in the sizes at which occur the rupture of growth line. The size range of this rupture in each sector is defined by the sizes of the "smallest mature specimen" and the "largest immature specimen". There is a high overlap of this size range between study sectors, difficulting, specimens identification to precise capture area if right chela size is used. More studies are needed to comprise geographic morphometric variations and to detect evolutive divergence features in relative growth of *L. antarcticus* stocks in the Magellan region.

L6 ANSWER 24 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1990:223971 BIOSIS
 DN PREV199089121261; BA89:121261
 TI MULTIVARIATE APPROACH TO GROUPING SOILS IN SMALL FIELDS II. SOIL GROUPING
 TECHNIQUE BY **CLUSTER** ANALYSIS.
 AU KOSAKI T [Reprint author]; JUO A S R
 CS DEP AGRO-ENVIRON SCI, OBIHIRO UNIV AGRIC VETERINARY MED, OBIHIRO 080, JPN
 SO Soil Science and Plant Nutrition, (1989) Vol. 35, No. 4, pp. 517-526.
 CODEN: SSPNAW. ISSN: 0038-0768.
 DT Article
 FS BA
 LA ENGLISH
 ED Entered STN: 10 May 1990
 Last Updated on STN: 10 May 1990
 AB **Cluster** analysis was applied in grouping soils based on their scores of the factors controlling soil variation in a cultivated, field at the Experimental Farm of the International Institute of Tropical Agriculture in Ibadan, Nigeria. The procedure employed here consisted of two steps: 1) grouping of the samples into a given number of provisional **clusters** through **non-hierarchical cluster** analysis, and 2) analysis of the similarity among those **clusters** using their means with **hierarchical cluster** analysis and determination of the proper number of the final **clusters**. Two initial settings in the assignment of the number of the provisional **clusters** were tested in **non-hierarchical cluster** analysis. Both trials gave a consistent classification, which also agreed with that based only on **hierarchical cluster** analysis. This combination of **non-hierarchical** and **hierarchical cluster** analyses enabled us to pressure a soil map solely based

on the factors controlling soil variation in the study area without introducing an a priori idea of soil classification. This method is not only an alternative to **hierarchical** clustering, but a more efficient tool in terms of capacity and computational speed to classify large numbers of samples which **hierarchical cluster** analysis is unable to handle.

L6 ANSWER 25 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1989:355631 BIOSIS
DN PREV198988047745; BA88:47745
TI MIDWATER FOOD WEB IN THE VICINITY OF A MARGINAL ICE ZONE IN THE WESTERN
WEDDELL SEA ANTARCTIC.
AU HOPKINS T L [Reprint author]; TORRES J J
CS DEP MARINE SCI, UNIV SOUTH FLORIDA, 140 7TH AVE SOUTH, ST PETERSBURG, FLA
33701, USA
SO Deep-Sea Research Part A Oceanographic Research Papers, (1989) Vol. 36,
No. 4, pp. 543-560.
CODEN: DRPPD5. ISSN: 0198-0149.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 2 Aug 1989
Last Updated on STN: 2 Aug 1989
AB The structure of the food web in the vicinity of a marginal ice zone was
investigated in the western Weddell Sea during austral autumn 1986. The
diets of 40 species of zooplankton and micronekton occurring in the
epipelagic zone were examined and compared using **non-**
hierarchical clustering procedures. Over half the species were in
three **clusters** of predominately small-particle (phytoplankton;
protozoans) grazers. These included biomass dominants *Calanoides acutus*,
Calanus propinquus, *Metridia gerlachei* and *Salpa thompsoni*. Six
clusters contained omnivores that had diets consisting of small
particles as well as a substantial fraction of metazoan food. Among these
was *Euphausia superba*. Seven groups were carnivorous, including species
of copepods (1), chaetognaths (3), and fishes (5). Copepods were the most
frequent food of carnivores; however krill also were important in the
diets of three fish species. Among small-particle grazers, phytoplankton
occurred more frequently in guts in individuals from open water; carnivory
was more in evidence in samples collected under the pack ice. Regional
comparisons of material taken on this and several previous cruises
indicate that, in most of the dominant species, diets remain relatively
consistent with respect to major food categories. Seasonal impact on
feeding dynamics appears to be great: the guts of grazing species were
generally much more full (visual evidence) during summer bloom conditions
than during the autumn. The following trophic sequence is suggested for
grazing zooplankton species in ice-covered regions of the Antarctic: (1)
Active small-particle grazing during the summer bloom period; (2) reduced
ingestion rates in autumn as primary production declines and the system
becomes more oligotrophic, with some species augmenting grazing with
carnivory; (3) descent of zooplankton biomass species into the mesopelagic
zone in late autumn-early winter with feeding largely terminated. The
sequence applies to the dominant zooplankton biomass species. Feeding
dynamics and vertical distribution of several of the important larger
sized grazing species, such as *Euphausia superba* and *Salpa thompsoni*,
remain largely unknown.

L6 ANSWER 26 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1989:294212 BIOSIS
 DN PREV198988019556; BA88:19556
 TI EVALUATION OF LOCAL COLLECTIONS OF WHEAT TRITICUM-SPP GERmplasm.
 AU GARG D K [Reprint author]; GAUTAM P L
 CS DEP AGRIC BOTANY, INST ADVANCED STUDIES, MEERUT UNIV, MEERUT-250005, UP,
 INDIA
 SO Genetica Agraria, (1988) Vol. 42, No. 3, pp. 255-262.
 CODEN: GEAGAC. ISSN: 0016-6685.
 DT Article
 FS BA
 LA ENGLISH
 ED Entered STN: 20 Jun 1989
 Last Updated on STN: 20 Jun 1989
 AB **Non-Hierarchical** Euclidean **cluster** analysis
 was used as a measure of genetic divergence among 377 Indian local wheat
 collections. Fifteen yield and yield contributing characters were used.
 All the collections were grouped into 15 different **clusters**
 showing the existence of high genetic diversity. **Cluster** 12 had
 the genotypes of high mean value for grain yield per plant.
 Shannon-Weaver diversity index (H') was used for working out genetic
 diversity among morphological characters. Maximum morphological variation
 (H' = 1.35) was observed in the collections from the hills of Uttar
 Pradesh (India). The germplasm collections with reasonable degree of
 resistance to rusts and powdery mildew were also identified.

L6 ANSWER 27 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1986:358846 BIOSIS
 DN PREV198682063320; BA82:63320
 TI **NON-HIERARCHICAL EUCLIDEAN CLUSTER ANALYSIS**
 IN CELERY.
 AU SETHI K L [Reprint author]; SAPRA R L
 CS NATL BUREAU PLANT GENETIC RESOURCES, NEW DELHI
 SO International Journal of Tropical Agriculture, (1986) Vol. 4, No. 1, pp.
 73-76.
 CODEN: IJTADD. ISSN: 0254-8755.
 DT Article
 FS BA
 LA ENGLISH
 ED Entered STN: 6 Sep 1986
 Last Updated on STN: 6 Sep 1986
 AB Genetic diversity studies were carried out and in celery the germplasm
 classification subjected to '**Non-Hierarchical**
 Euclidean **Cluster** Analysis' taking into consideration the
 variation explained by all the eigen roots using the method of Beale
 (1969). The percentage of variation explained with the help of two eigen
 roots was only 64.66 per cent and not sufficient to follow the graphical
 approach in two dimensional spaces.

L6 ANSWER 28 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1986:150785 BIOSIS
 DN PREV198681061201; BA81:61201
 TI FOOD WEB OF AN ANTARCTIC MIDWATER ECOSYSTEM.
 AU HOPKINS T L [Reprint author]
 CS DEP MARINE SCI, UNIV SOUTH FLA, ST PETERSBURG, FL 33701, USA
 SO Marine Biology (Berlin), (1985) Vol. 89, No. 2, pp. 197-212.

CODEN: MBIOAJ. ISSN: 0025-3162.

DT Article

FS BA

LA ENGLISH

ED Entered STN: 25 Apr 1986

Last Updated on STN: 25 Apr 1986

AB The diets of 93 species of plankton and micronekton taken in the upper 1000 m of Crocker Passage (Gerlache Strait) in the austral fall, 1983, were examined and the principal features of the food web were characterized. Most species were small particle feeders, with phytoplankton and debris (of phytoplankton and krill) being the principal diet components. Krill remains were found in the guts of the majority of species examined, with the krill playing a greater role in the form of molts and debris than as living prey. Carnivores fed mostly on copepods, coelenterates and salps. Some of the larger species fed on live krill.

Non-hierarchical cluster analysis of diet

information supported the concept of resource partitioning and determined the arrangement of the species into 21 feeding groups. **Cluster** analysis groupings tended to be along genetic lines with closely related and morphologically similar species having similar diets. These analyses were based on collections made in the austral fall (March-April, 1983) when phytoplankton standing crop was low, most zooplankton species had descended into the mesopelagic zone, and some of the more abundant species, such as *Calanoides acutus*, had ceased feeding. Because the trophodynamics of Antarctic ecosystems is strongly pulse-induced, it is essential to examine the food web at different periods in the seasonal cycle.

L6 ANSWER 29 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1985:240354 BIOSIS

DN PREV198579020350; BA79:20350

TI PLANKTONIC COPEPODS IN THE LAGOON OF NEW-CALEDONIA ECOLOGICAL FACTORS AND SPECIES ASSEMBLAGES.

AU BINET D [Reprint author]

CS ANTENNE ORSTOM, CENTRE OCEANOLOGIQUE DE BRETAGNE, BP 337, F-29273, BREST CEDEX, FRANCE

SO Marine Biology (Berlin), (1984) Vol. 82, No. 2, pp. 143-156.

CODEN: MBIOAJ. ISSN: 0025-3162.

DT Article

FS BA

LA FRENCH

AB In the southwestern part of the lagoon of New Caledonia (South Pacific Ocean), a plankton sampling program was conducted from Feb. 1978 to April 1979. During 11 cruises, 5 stations in the open sea and various bays were sampled at approximately monthly intervals. A transect of 3 stations (mid-lagoon, near-reef and barrier-reef channel), visited every 2 wk, completed the sampling program. The 52 most abundant copepod species were analyzed for seasonal and regional variations. Cruise and transect data, dealt with separately, were analyzed in a variety of ways. Correspondence analyses (reciprocal averaging) of qualitative and quantitative copepod counts were made. Species partition was achieved by 2 successive methods: **non-hierarchical**, followed by **hierarchical** classification. Between-species distance was computed from their coordinates on the factorial axis. Species **clusters** obtained were plotted in the factorial planes to assess ecological preferences. The main ecological factors appear to be spatial patterns, seasonal

temperature cycle, and changes in wind force and direction. Different populations inhabit the open sea, near-reef, mid-lagoon, shallow and deep-bay waters. *Acartia australis* outnumbers all other species in the reef vicinity. *A. amboinensis* is the most abundant in the deep, fjord-like bay. *Canthocalanus pauper*, *Paracalanus parvus*, *Bestiola* sp., *Centropages orsinii* and *A. bispinosa* are characteristic of shallow bays. Seasonal barycenters appear close to some station barycenters: summer close to mid-lagoon, winter close to open sea, and spring close to near-reef barycenters, respectively. This may be explained by the seasonal dynamics of the lagoon water. Variations of plankton populations and biomass in the lagoon seem to be governed by the direction of water flow across the reef channels. Enrichment factors are terrestrial sediment wash-out after rainfall and, probably, trade wind-induced upwelling.

L6 ANSWER 30 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1984:337831 BIOSIS
DN PREV198478074311; BA78:74311
TI DISSOLVED OXYGEN CONCENTRATIONS IN LAKE ERIE USA CANADA 1. STUDY OF
SPATIAL AND TEMPORAL VARIABILITY USING **CLUSTER** AND REGRESSION
ANALYSIS.
AU ANDERSON J E [Reprint author]; EL-SHAARAWI A H; ESTERBY S R; UNNY T E
CS DEP OF CIVIL ENGINEERING, UNIV OF WATERLOO, WATERLOO, ONT N2L 3G1, CANADA
SO Journal of Hydrology (Amsterdam), (1984) Vol. 72, No. 3-4, pp. 209-230.
CODEN: JHYDA7. ISSN: 0022-1694.
DT Article
FS BA
LA ENGLISH
AB A **non-hierarchical** nearest-centroid clustering method
was used to separate data pairs consisting of the dissolved oxygen (DO)
concentration and temperature into 4 groups corresponding to hypolimnetic
and non-hypolimnetic water of the Central and Eastern Basins of Lake Erie.
For the stations which were common to all cruises within a year and were
classified as being in the hypolimnion, initial DO concentrations and
depletion rates were calculated and tests about their constancy were
performed using weighted regression analysis and regression models with
the time structure of the data explicitly incorporated in the models. The
yearly uncorrected depletion rates for 1967-1980 were similar to values
previously reported by several authors, indicating that this
semi-objective clustering procedure provides a practical alternative to
subjective selection of data. The conclusions about constancy of initial
concentraitons and depletion rates based on an unweighted regression
analysis were shown to differ from those of weighted regression. Using
regression with empirical weights, neither the initial DO concentration
nor the depletion rate remained constant between 1967 and 1980 in the
Central Basin but the depletion rate remained constant and the initial DO
concentration varied in the Eastern Basin.

L6 ANSWER 31 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1982:149074 BIOSIS
DN PREV198273009058; BA73:9058
TI **HIERARCHICAL** CLASSIFICATION OF COMMUNITY DATA.
AU GAUCH H G JR [Reprint author]; WHITTAKER R H
CS SECTION OF ECOLOGY SYSTEMATICS, CORNELL UNIV, ITHACA, NEW YORK 14850, USA
SO Journal of Ecology, (1981) Vol. 69, No. 2, pp. 537-558.
CODEN: JECOAB. ISSN: 0022-0477.

DT Article
FS BA
LA ENGLISH
AB The application of **hierarchical** classification to ecological community data is examined, using a variety of classification techniques and test data sets. Problems discussed include the choice of a conceptual space in which points representing samples or species or both are located; the effects of random noise and nonlinearity; the degree to which **clusters** are natural to a data set or are imposed by the clustering technique; the choice of criteria for locating divisions; clustering strategies (**non-hierarchical** vs. **hierarchical**, divisive vs. agglomerative and polythetic vs. monothetic); the presentation of results of various clustering techniques; and methods for evaluating and comparing clustering techniques and their results. Five **hierarchical** clustering techniques are compared: complete linkage clustering, the unweighted pair group method using arithmetic averages, minimization of within-group dispersion, 2-way indicator species analysis, and partitioning of an ordination space (using detrended correspondence analysis, a modification of reciprocal averaging). The first 3 techniques are agglomerative and the last 2 are divisive. Data sets for tests include simulated data sets in 1 to 4 dimensions (some incorporating noise of 3 kinds), and field data varying in number of samples, noise level and number and length of community gradients. Two-way indicator species analysis is usually the best, but there are cases in which other techniques may be complementary or superior. Theoretical requirements and test results are discussed to show why clustering of ecological community data is usually best approached by a divisive strategy. This conclusion is important because the analysis may be stopped after a limited number of divisions, thus needing less computation than do agglomerative strategies. The 2 divisive techniques discussed here have computer requirements which rise only linearly with the amount of data, making analysis of large data sets practical.

L6 ANSWER 32 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1981:241753 BIOSIS
DN PREV198172026737; BA72:26737
TI THE IDENTIFICATION OF STRUCTURES IN CONNECTION MATRICES OF PALMAR DERMATOGLYPHIC VARIABLES.

AU DENNIS R L H [Reprint author]; SUNDERLAND E
CS DEP OF ANTHROPOLOGY, UNIV OF DURHAM, SOUTH END HOUSE, SOUTH ROAD, DURHAM DH1 3TG ENGLAND, UK

SO Acta Anthropogenetica, (1979) Vol. 3, No. 3-4, pp. 93-126.
CODEN: ACANDO. ISSN: 0258-0357.

DT Article
FS BA
LA ENGLISH

AB Structure-seeking techniques were applied to dermatoglyphic variables from samples of human populations in the North Pennine Dales, northern England [UK], including 1624 males and 1788 females. Results of multivariate analyses on 50 palmar variables are included; details on the fingers were reported earlier. Previous work disclosed low associations between palm and finger variables. The palmar variables include 3 interdigital ridge counts, 13 topological patterns, deltas ef, t, t', t" and tb and the 4 mainlines A, B, C and D for each hand. Two ordinal coding schemes were used for the mainlines in order to process blind terminations of the proximal radiants. A nascent scheme treats blind terminations of lines as

embryonic and of low rank; a sequential scheme interprets them as acute reflections of the proximal radiants to source, attributing to them a correspondingly higher rank. Analyses have been effected by way of non-metric scaling algorithms and factoring techniques on ordinal connection matrices for each sex. Solutions are displayed as non-metric 2-dimensional scaling plots of the variables on which are superimposed **non-hierarchical** partially overlapping **clusters** of varimax rotated factors. Results are in agreement for nascent and sequential coding schemes depicting 11 non-overlapping and 3 overlapping **clusters**. The latter comprise interdigital variables, namely lines B, C and D, patterns III, IIIT and IV and ridge count bc. Subsequent ordination revealed consistent relationships in this group, clear variable homolog linkages and distinct bilateral **clusters**; and a distinctly less compact assortment of left hand as opposed to right hand variables.

LG ANSWER 33 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 1980:183429 BIOSIS
 DN PREV198069058425; BA69:58425
 TI DISTRIBUTION OF WESTERN BEAUFORT SEA ALASKA USA POLYCHAETOUS ANNELIDS.
 AU BILYARD G R [Reprint author]; CAREY A G JR
 CS SCH OCEANOGR, OREG STATE UNIV, CORVALLIS, OREG 97331, USA
 SO Marine Biology (Berlin), (1979) Vol. 54, No. 4, pp. 329-340.
 CODEN: MBIOAJ. ISSN: 0025-3162.

DT Article
 FS BA
 LA ENGLISH

AB Depth and depth-related processes appear to exert primary control over the distributional patterns of species of polychaetous annelids in the western Beaufort Sea (Cape Halkett-Barter Island, Alaska). Species richness and total polychaete abundance are maximal along the outer continental shelf and upper continental slope. Stations exhibiting the most similar polychaete assemblages are located at similar depths. Some species distributions appear to correlate better with sediment type than with depth. Maximum abundance occurs deeper on the continental slope to the west; and station **clusters** generated by **non-hierarchical** clustering (using the dominant polychaete species data) are not sorted strictly by depth. In a canonical analysis of discriminance, the station **clusters** were projected onto a 2 dimensional plane in species space. The 1st and 2nd canonical variables of the station **clusters** correlate with sediment grain-size distributions, suggesting a relationship between polychaete distribution patterns and the sedimentary environment. This relationship is further substantiated when sediment grain-size distributions for each station are plotted on a tertiary diagram: the stations are grouped and ordered in a pattern similar to that generated by the canonical analysis of discriminance.

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<input type="checkbox"/>	L2	L1 same cluster\$	67
<input type="checkbox"/>	L1	hierarchical same non-hierarchical	988

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